

178/550

FIGURE 178

MPCAQRSWLANLSVVAQLLNFGALCYGRQPQPGPVRFPDRRQEHFIKGLPEYHVVG PVRVDAS
GHFLSYGLHYPITSSRRKRDLGSEDWVYYRISHEEKDLFFNLTVNQGFLSNSYIMEKRYGNL
SHVKMMASSAPLCHLSGTVLQQGTRVGTAALSACHGLTGFFQLPHGDDFFIEPVKKHPLVEGGY
HPHIVYRRQKVPETKEPTCGLKGIVTHMSSWVEESVLFFW

Signal peptide:

amino acids 1-27

N-glycosylation sites.

amino acids 11-15, 105-109, 125-129

N-myristoylation site.

amino acids 149-155

179/550

FIGURE 179

CAGATTTAAAAAGAAAACCTTTACTGAATCAGCTGAGTGTTAATAATACGAATTTCTTTCT
TGCCAATTCTGATCTGAACAGAAAATCCAAGAACAGGGATATGTGTGGATTACAGTTTTCTCT
GCCTTGCCCTACGACTGTTTCTGGTTGTTACCTGTTATCTTTTATTATTACTCCACAAAGAAAT
ACTTGGATGTTCTGCTCTGTTTGTCTGAGCTCTGCACTGGGAGACAAATTAAGTCCGTAACCTTAGG
CCTTTTCGAGTATTCCCTAAGAATTTTCTGAAAGTACAGTTTTTCTGTATCTGACTGGGAATAA
TATATCTTATATAAATGAAAGTGAATTAACAGGACTTCATTCTCTTGTAGCATTGTATTTGGA
TAATCTAACATTCTGTATGTATATCCAAAAGCCTTTGTTCAATTGAGGCATCTATATTTTCT
ATTTCTAAATAATAATTTTCATCAAACGCTTAGATCCTGGAATATTTAAGGGACTTTTAAATCT
TCGTAATTTATATTTACAGTATAATCAGGTATCTTTTGTTCGAGAGGAGTATTTAATGATCT
AGTTTCAGTTCAGTACTTAAATCTACAAAGGAATCGCCTCACTGTCCTTGGGAGTGGTACCTT
TGTTGGTATGGTTGCTCTTCGGTACTTGATTTATCAAACAATAACATTTTGAGGATATCAGA
ATCAGGCTTTCAACATCTTGAAAACCTTGCTTGTTTGTATTTAGGAAGTAATAATTTAACAAA
AGTACCATCAAATGCCTTTGAAGTACTTAAAAGTCTTAGAAGACTTTCTTTGTCTCATAATCC
TATTGAAGCAATACAGCCCTTTGCATTTAAAGGACTTGCCAATCTGGAATACCTCCTCCTGAA
AAATTCAAGAATTAGGAATGTTACTAGGGATGGGTTTAGTGGAATTAATAATCTTAAACATTT
GATCTTAAGTCATAATGATTTAGAGAATTTAAATCTGACACATTCAGTTTGTTAAAGAATTT
AATTTACCTTAAGTTAGATAGAAACAGAATAATTAGCATTGATAATGATACATTTGAAAATAT
GGGAGCATCTTTGAAGATCCTTAATCTGTCATTTAATAATCTTACAGCCTTGCAATCCAAGGGT
CCTTAAGCCGTTGTCTTCATTGATTTCATCTTCAGGCAAATCTAATCCTTGGGAATGTAACTG
CAAACCTTTTGGGCCTTCGAGACTGGCTAGCATCTTCAGCCATTACTCTAAACATCTATTGTCA
GAATCCCCCATCCATGCGTGGCAGAGCATTACGTTATATTAACATTACAAATTGTGTTACATC
TTCAATAAATGTATCCAGAGCTTGGGCTGTTGTAAAATCTCCTCATATTCATCACAAGACTAC
TGCGCTAATGATGGCCTGGCATAAAGTAACCACAAATGGCAGTCCTCTGGAAAATACTGAGAC
TGAGAACATTACTTTCTGGGAACGAATTCCTACTTCACCTGCTGGTAGATTTTTTCAAGAGAA
TGCCCTTTGGTAATCCATTAGAGACTACAGCAGTGTTACCTGTGCAAATACAACCTTACTACTTC
TGTTACCTTGAACCTTGGAACAAAACAGTGCTCTACCGAATGATGCTGCTTCAATGTCAGGGAA
AACATCTCTAATTTGTACACAAGAAGTTGAGAAGTTGAATGAGGCTTTTGACATTTTGCTAGC
TTTTTTCATCTTAGCTTGTTGTTTAAATCATTTTTTTGATCTACAAAGTTGTTCAGTTTAAACA
AAAACCTAAAGGCATCAGAAAACCTCAAGGGAAAATAGACTTGAATACTACAGCTTTTATCAGTC
AGCAAGGTATAATGTAACCTGCCTCAATTTGTAACACTTCCCCAAATCTCTAGAAAGTCCTGG
CTTGGAGCAGATTCGACTTCATAAACAAATTGTTCTGAAAATGAGGCACAGGTCATTCTTTT
TGAACATTCTGCTTTATTAACTCAACTAAATATTGTCTATAAGAACTTCAGTGCCATGGACAT
GATTTAACTGAAACCTCCTTATATAATTATATACTTTAGTTGGAATATAATGAATTATATG
AGGTTAGCATTATTAAATATGTTTTTTNTTAAAAAAAAAAAAAAAAAAAAAAAAA

180/550

FIGURE 180

MCGLQFSLPCLRLFLVVTCYLLLLLLHKEILGCSSVCQLCTGRQINCRNLGLSSIPKNFPPESTV
FLYLTGNNISYINESELTGLHSLVALYLDNSNILEYVYPKAFVQLRHLYFLFLNNNFIKRLDPG
IFKGLLNLRNLYLQYNQVSFVPRGVFNDLVSQYLNLRNRLTVLGSGTFVGMVALRILDLSN
NNILRISESGFQHLENLACLYLGSNNLTKVPSNAFEVLKSLRRLSLSHNPICAIQPFQFAFKGLA
NLEYLLLKNSRIRNVTRDGFSGINNLKHLILSHNDLENLNSDTFSLLKNLIYKLDNRNIISI
DNDTFENMGASLKILNLSFNNLTALHPRVLKPLSSLIHLQANSNPWECNCKLLGLRDWLASSA
ITLNIYCQNFPSPMRGRALRYINITNCVTSSINVSRAWAVVKSPHIIHKTTALMMAWHKVTNG
SPLENTETENITFWERIPTSPAGRFFQENAFGNPLETTAVLPVQIQLTTSVTLNLEKNSALPN
DAASMSGKTSLECTQEVEKLNEAFDILLAFFILACVLIIFLIYKVVQFKQKLKASENSRENRL
EYYSFYQSARYNVTASICNTSPNSLESPGLEQIRLHKQIVFENEAQVILFEHSAL

Signal peptide:

amino acids 1-41

Transmembrane domain:

amino acids 530-547

N-glycosylation sites.amino acids 71-75, 76-80, 215-219, 266-270, 317-321, 331-335,
336-340, 400-404, 410-414, 451-455, 579-583**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 231-235

N-myristoylation sites.

amino acids 3-9, 69-75, 126-132, 174-180

ATP/GTP-binding site motif A (P-loop).

amino acids 506-514

181/550

FIGURE 181

GGCCTGGCGCGGCGCTCCGGTAAGGCGTGTGTGCGGCAGGGCGGGGACAGAACCGTCCTCTCG
GGCTCTGGGCGTGTCCGAGACCGCGCTCCCCGCCGAAATCAAGCTCCGAGTCATCCGTGTGGG
GCATTTCGTCCCCCTGGCACAGTTGGCCTCTTCCAGAAGCCCGTTTTGTTTGTTTTACGTCT
AAATTCGCGTCGGTTCTTATTTCTCTCCCTGGCAAGGTCTGAAGACGGGTAGGAGAATAACCT
GTGTCAGCGTGT~~TATG~~ATGCCGTCCCGTACCAACCTGGCTACTGGAATCCCCAGTAGTAAAGT
GAAATATTCAAGGCTCTCCAGCACAGACGATGGCTACATTGACCTTCAGTTTAAGAAAACCCC
TCCTAAGATCCCTTATAAGGCCATCGCACTTGCCACTGTGCTGTTTTTTGATTGGCGCCTTCT
CATTATTATAGGCTCCCTCCTGCTGTCAGGCTACATCAGCAAAGGGGGGGCAGACCGGGCCGT
TCCAGTGCTGATCATTGGCATTCTGGTGTTCTACCCGGATTTTACCACCTGCGCATCGCTTA
CTATGCATCCAAAGGCTACCGTGGTTACTCCTATGATGACATTCCAGACTTTGATGAC~~TAG~~CA
CCCACCCCATAGCTGAGGAGGAGTCACAGTGGAAGTGTCCCAGCTTTAAGATATCTAGCAGAA
ACTATAGCTGAGGACTAAGGAATTCTGCAGCTTGCAGATGTTTAAGAAAATAATGGCCAGATT
TTTTGGGTCCTTCCCAAAGATGTTAAGTGAACCTACAGTTAGCTAATTAGGACAAGCTCTATT
TTTCATCCCTGGGCCCCTGACAAGTTTTTCCACAGGAATATGTATCATGGAAGAATAGAGGTTA
TTCTGTAATGGAAAAGTGTGCTGCCACCACCCTCTGTAGAGCTGAGCATTTCTTTTAAATA
GTCTTCATTGCCAATTTGTTCTTGTAGCAAATGGAACAATGTGGTATGGCTAATTTCTTATTA
TTAAGTAGTTTATTTTAAAAATATCTGAGTATATTATCCTGTACACTTATCCCTACCTTCATG
TTCCAGTGGAAGACCTTAGTAAAATCAAAGATCAGTGAGTTCATCTGTAATATTTTTTTTACT
TGCTTTCTTACTGACAGCAACCAGGAATTTTTTTATCCTGCAGAGCAAGTTTCAAATGTAA
ATACTTCCTCTGTTTAAACAGTCCTTGGACCATTCTGATCCAGTTCACCAGTAGGTTGGACAGC
ATATAATTTGCATCATTTTGTCCCTTGTAATCAAGATGTTCTGCAGATTATTCCTTTAACGG
CCGGACTTTTGGCTGTTTCCTAATGAAACATGTAGTGTTATTATTATAGAGTTTATAGCCGTA
TTGCTAGCACCTTGTAGTATGTCATCATTCTGCTCATGATTCCAAGGATCAGCCTGGATGCCT
AGAGGACTAGATCACCTTAGTTTGATTCTATTTTTTTAGCTTGCAAAAAGTGACTTATATCCA
AAGAAATTAAATGTTGAAATCCAAATCCTAGAAATAAATGAGTTTNNNTCCAAAAA
AAA

182/550

FIGURE 182

MMPSRTNLATGIPSSKVKYSRLSSTDGYYDLQFKKTPPKIPYKAIALATVLFLLGAFLIIIG
SLLLSGYISKGGADRAVPVLIIGILVFLPGFYHLRIAYYASKGYRGYSYDDIPDFDD

Transmembrane domains:

amino acids 45-66, 79-95

N-myristoylation sites.

amino acids 11-17, 75-81

FIGURE 183

[illegible]

184/550

FIGURE 184

QCCRKIKDTVQKLASDHKDIHSSVSRVGKAIDRNFDSEICGVVSDAVWDAREQQQQIILQMAIV
EHLYQQGMLSVAEELCQESTLNVDLDFKQPFLELNRILEALHEQDLGPALEWAVSHRQRLEL
NSSLEFKLHRLHFIRLLAGGPAKQLEALSYARHFQPFARLHQREIQVMMGSLVYLRLGLEKSP
YCHLLDSSHWAEICETFTRDACSLGLSVESPLSVSFASGCVALPVLNMIKAVIEQRQCTGVW
N HKDELPIEIELGMKCWYHSVFACPI LRQQTSDSNPPIKLCGHVISRDALNKLINGGKLCPC
YCPMEQNPADGKRIIF

Transmembrane domain:

amino acids 222-241

N-glycosylation site.

amino acids 129-133

Tyrosine kinase phosphorylation site.

amino acids 151-159, 184-193

Amidation site.

amino acids 327-331

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 222-233

185/550

FIGURE 185

GAGCGACGCTGTCTCTAGTCGCTGATCCCAAATGCACCGGCTCATCTTTGTCTACACTCTAAT
CTGCGCAAACCTTTTGCAGCTGTCGGGACACTTCTGCAACCCCGCAGAGCGCATCCATCAAAGC
TTTGCGCAACGCCAACCTCAGGCGAGATGACTTGTACCGAAGAGATGAGACCATCCAGGTGAA
AGGAAACGGCTACGTGCAGAGTCCTAGATTCCCGAACAGCTACCCCAGGAACCTGCTCCTGAC
ATGGCGGCTTCACTCTCAGGAGAATACACGGATACAGCTAGTGTTTGACAATCAGTTTGGATT
AGAGGAAGCAGAAAATGATATCTGTAGGTATGATTTTGTGGAAGTTGAAGATATATCCGAAAC
CAGTACCATTTATTAGAGGACGATGGTGTGGACACAAGGAAGTTCCTCCAAGGATAAAATCAAG
AACGAACCAAATTAAAATCACATTCAAGTCCGATGACTACTTTGTGGCTAAACCTGGATTCAA
GATTTATTATTCTTTGCTGGAAGATTTCCAACCCGCAGCAGCTTCAGAGACCAACTGGGAATC
TGTCACAAGCTCTATTTTCAGGGGTATCCTATAACTCTCCATCAGTAACGGATCCCACTCTGAT
TGCGGATGCTCTGGACAAAAAATTGCAGAATTTGATACAGTGGAAGATCTGCTCAAGTACTT
CAATCCAGAGTCATGGCAAGAAGATCTTGAGAATATGTATCTGGACACCCCTCGGTATCGAGG
CAGGTCATACCATGACCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAGCG
TTACAGTTGCACTCCCAGGAATTACTCGGTCAATATAAGAGAAGAGCTGAAGTTGGCCAATGT
GGTCTTCTTTCCACGTTGCCTCCTCGTGCAGCGCTGTGGAGGAAATTGTGGCTGTGGAAGTGT
CAACTGGAGGTCCTGCACATGCAATTCAGGGAAAACCGTGAAAAAGTATCATGAGGTATTACA
GTTTGAGCCTGGCCACATCAAGAGGAGGGGTAGAGCTAAGACCATGGCTCTAGTTGACATCCA
GTTGGATCACCATGAACGATGCGATTGTATCTGCAGCTCAAGACCACCTCGATTAAGAGAATGT
GCACATCCTTACATTAAGCCTGAGAGAA

186/550

FIGURE 186

MHRLIFVYTLICANFCSCRDTSATPQSASIKALRNANLRRDDLYRRDETIQVKGNQYVQSPRF
PNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLEEAENDICRYDFVEVEDISETSTIIRGRWCG
HKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYSLLEDFQPAAASETNWESVTSSISGVSY
NSPSVTDPTLIADALDKKIAEFDTVEDLLKYFNPESWQEDLENMYLDTPRYRGRSYHDRKSKV
DLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFPRCLLVQRCGGNCGCGTVNWRSCTCNSG
KTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERCDCICSSRPPR

Signal peptide:

amino acids 1-18

N-glycosylation site.

amino acids 270-274

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 262-266

Tyrosine kinase phosphorylation site.

amino acids 256-265

N-myristoylation sites.

amino acids 94-100, 186-192, 297-303, 298-304

TonB-dependent receptor proteins signature 1.

amino acids 1-56

187/550

FIGURE 187

CATGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGGCGCCTTGGGGACGGGCAGTTCCTTG
TGTCTCTGGTGGTTTGCCTAAACCTGCAAACATCACCTTCTTATCCATCAACATGAAGAATGT
CCTACAATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATTT
CATATATGGGCAAAAGAAATGGCTGAATAAATCAGAATGCAGAAATATCAATAGAACCTACTG
TGATCTTTCTGCTGAACTTCTGACTACGAACACCAGTATTATGCCAAAGTTAAGGCCATTTG
GGGAACAAAGTGTTCCAAATGGGCTGAAAGTGGACGGTCTATCCTTTTTTAGAAACACAAAT
TGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGTCTTGACAGCTCC
AGAGAAGTGGAAGAGAAATCCAGAAGACCTTCTGTTTCCATGCAACAAATATACTCCAATCT
GAAGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAACGTGGTCCCAGTGTGTGACCAA
CCACACGCTGGTGCTCACCTGGCTGGAGCCGAACACTCTTTACTGCGTACACGTGGAGTCCTT
CGTCCCAGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTGCCAGGACTTTGAAAGA
TCAATCATCAGAGTTCAAGGCTAAAATCATCTTCTGGTATGTTTTGCCATATCTATTACCGT
GTTTCTTTTTTCTGTGATGGGCTATTCCATCTACCGATATATCCACGTTGGCAAAGAGAAACA
CCCAGCAAATTTGATTTTGATTTATGGAAATGAATTTGACAAAAGATTCTTTGTGCCTGCTGA
AAAAATCGTGATTAACCTTTATCACCTCAATATCTCGGATGATTCTAAAATTTCTCATCAGGA
TATGAGTTTACTGGGAAAAAGCAGTGATGTATCCAGCCTTAATGATCCTCAGCCCAGCGGGAA
CCTGAGGCCCCCTCAGGAGGAAGAGGAGGTGAAACATTTAGGGTATGCTTCGCATTTGATGGA
AATTTTTTGTGACTCTGAAGAAAACACGGAAGGTACTTCTCTCACCCAGCAAGAGTCCCTCAG
CAGAACAATACCCCCGGATAAAACAGTCATTGAATATGAATATGATGTCAGAACCCTGACAT
TTGTGCGGGGCCTGAAGAGCAGGAGCTCAGTTTGCAGGAGGAGGTGTCCACACAAGGAACATT
ATTGGAGTCGCAGGCAGCGTTGGCAGTCTTGGGCCCCGAAACGTTACAGTACTCATACACCCC
TCAGCTCCAAGACTTAGACCCCCTGGCGCAGGAGCACACAGACTCGGAGGAGGGGGCCGGAGGA
AGAGCCATCGACGACCCTGGTCGACTGGGATCCCCAACTGGCAGGCTGTGTATTCTTCGCT
GTCCAGCTTCGACCAGGATTCAGAGGGCTGCGAGCCTTCTGAGGGGGATGGGCTCGGAGAGGA
GGGTCTTCTATCTAGACTCTATGAGGAGCCGGCTCCAGACAGGCCACCAGGAGAAAATGAAAC
CTATCTCATGCAATTCATGGAGGAATGGGGGTATATGTGCAGATGGAAAAC**TGAT**GCCAACA
CTTCCTTTTGCCTTTTGTTTCCTGTGCAAACAAGTGAGTCACCCCTTTGATCCCAGCCATAAA
GTACCTGGGATGAAAGAAGTTTTTTCCAGTTTGTGTCAGTGTCTGTGAGAA

188/550

FIGURE 188

MPLPPLLLLLLLAAPWGRAVPCVSGGLPKPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYF
IYGQKKWLNKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAESGRFYFPFLETQI
GPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVLNTKSNRTWSQCVTN
HTLVLTWLEPNTLYCVHVESFVPGPPRAQPSEKQCARTLKDQSSEFKAKIIFWYVLPISITV
FLFSVMGYSIYRYIHVGKEKHHPANLILYIGNEFDKRFFVPAEKIVINFITLNISSDDSKISHQD
MSLLGKSSDVSSLNDPQPSGNLRPPQEEEEVKHLGYASHLMEIFCDSEENTEGTSLTQQESLS
RTIPDPKTVIEYEYDVRTTDCAGPEEQELSLQEEVSTQGTLLSQAALAVLGPQTLQYSYTP
QLQDLDPPLAQEHTDSEEGPEEEPPSTTLVDWDPQTGRLCIPLSSFDQDSEGCEPSEGDLGEE
GLLSRLYEPPAPDRPPGENETYLMQFMEEWGLYVQMEN

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 240-260

N-glycosylation sites.amino acids 31-34, 72-75, 80-83, 171-174, 180-183, 189-192,
304-307, 523-526**Tyrosine kinase phosphorylation site.**

amino acids 385-392, 518-526

N-myristoylation sites.

amino acids 53-58, 106-111, 368-373, 492-497

Tissue factor

amino acids 1-278

189/550

FIGURE 189

ATGTGCTGCTGGCCGCTGCTCCTGCTGTGGGGGCTGCTCCCCGGGACGGCGGGCGGGGGGCTCG
GGCCGAACCTATCCGCACCGGACCCTCCTGGACTCGGAGGGCAAGTACTGGCTGGGCTGGAGC
CAGCGGGGCAGCCAGATCGCCTTCCGCCTCCAGGTGCGCACTGCAGGCTACGTGGGCTTCGGC
TTCTCGCCCACCGGGGCCATGGCGTCCGCGGACATCGTTCGTGGGCGGGGTGGCCACGGGCGG
CCCTACCTCCAGGATTATTTTACAAATGCAAATAGAGAGTTGAAAAAAGATGCTCAGCAAGAT
TACCATCTAGAATATGCCATGGAAAATAGCACACACAATAATTGAATTTACCAGAGAGCTG
CATACATGTGACATAAATGACAAGAGTATAACGGATAGCACTGTGAGAGTGATCTGGGCCTAC
CACCATGAAGATGCAGGAGAAGCTGGTCCCAAGTACCATGACTCCAATAGGGGCACCAAGAGT
TTGCGGTTATTGAATCCTGAGAAAAGTAGTGTGCTATCTACAGCCTTACCATACTTTGATCTG
GTAAATCAGGACGTCCCCATCCCAAACAAAGATACAACATATTGGTGCCAAATGTTTAAGATT
CCTGTGTTCCAAGAAAAGCATCATGTAATAAAGGTTGAGCCAGTGATACAGAGAGGCCATGAG
AGTCTGGTGCACCACATCCTGCTCTATCAGTGCAGCAACAACCTTTAACGACAGCGTTCTGGAG
TCCGGCCACGAGTGCTATCACCCCAACATGCCCGATGCATTCTCTACCTGTGAAACTGTGATT
TTTGCTGGGCTATTGGTGGAGAGGGGCTTTTCTTATCCACCTCATGTTGGATTATCCCTTGGC
ACTCCATTAGATCCGCATTATGTGCTCCTAGAAGTCCATTATGATAATCCCACTTATGAGGAA
GGCTTAATAGATAATTCTGGACTGAGGTTATTTTACACAATGGATATAAGGAAATATGATGCT
GGGGTGATTGAGGCTGGCCTCTGGGTGAGCCTCTTCCATACCATCCCTCCAGGGATGCCTGAG
TTCCAGTCTGAGGGTCACTGCACTTTGGAGTGCCTGGAAGAGGCTCTGGAAGCCGAAAAGCCA
AGTGGAAATTCATGTGTTTGCTGTTCTTCTCCATGCTCACCTGGCTGGCAGAGGCATCAGGCTG
CGTCATTTTCGAAAAGGGAAGGAAATGAAATTAAGTGCCTATGATGATGATTTTGACTTCAAT
TTCCAGGAGTTTCAGTATCTAAAGGAAGAACAAACAATCTTACCAGGAGATAACCTAATTACT
GAGTGTCGCTACAACACGAAAGATAGAGCTGAGATGACTTGGGGAGGACTAAGCACCAGGAGT
GAAATGTGTCTCTCATACCTTCTTTATTACCCAAGAATTAATCTTACTCGATGTGCAAGTATT
CCAGACATTATGGAACAACCTTCAGTTCATTGGGGTTAAGGAGATCTACAGACCAGTCACGACC
TGGCCTTTTATTATCAAAAGTCCCAAGCAATATAAAAACCTTTCTTTCATGGATGCTATGAAT
AAGTTTAAATGGACTAAAAAGGAAGGTCTCTCCTTCAACAAGCTGGTCCTCAGCCTGCCAGTG
AATGTGAGATGTTCCAAGACAGACAATGCTGAGTGGTCGATTCAAGGAATGACAGCATTACCT
CCAGATATAGAAAGACCTTATAAAGCAGAACCTTTGGTGTGTGGCACGTCTTCTTCTCTTCC
CTGCACAGAGATTTCTCCATCAACTTGCTTGTGTTTGCCTTCTGCTACTCAGCTGCACGCTGAGC
ACCAAGAGCTTG**TGAT**CAAAATTTCTGTTGGACTTGACAATGTTTTCTATGATCTGAACCTGTC
ATTTGAAGTACAGGTTAAAGACTGTGTCCACTTTGGGCATGAAGAGTGTGGAGACTTTTCTTC
CCATTTTCCCTCCCTCCTTTTTCCTTTCCATGTTACATGAGAGACATCAATCAGGTTCTCTT
CTCTTTCTTAGAAATACCTGATGTTATATATACATGGTCAATAAAATAAACTGGCCTGACTT
AAGATAACCATTTTAAAAAATTGGGCTGTCATGTGGGAATAAAAGAATTCTTTCTTCTTCTAAA
AAAAAAA

190/550

FIGURE 190

MCCWPLLLLWGLLPGTAAGGSGRTYPHRTLDDSEGKYWLGWSQRGSQIAFRLQVRTAGYVGFG
ESPTGAMASADIVVGGVAHGRPYLQDYFTNANRELKKDAQQDYHLEYAMENSTHTIIEFTREL
HTCDINDKSITDSTVRVIWAYHHEDAGEAGPKYHDSNRGTKSLRLLNPEKTSVLSTALPYFDL
VNQDVPIPNKDTTYWCQMFKIPVFQEKHHVIKVEPVIIQRGHESLVHHILLYQCSNNFNDSVLE
SGHECYHPNMPDAFLTCTETVIFAWAIGGEGFSYPPHVGLSLGTPLDPHYVLLLEVHYDNPTYEE
GLIDNSGLRLFYTMDIRKYDAGVIEAGLWVSLFHTIPPGMPEFQSEGHCTLECLEEAELEAERP
SGIHVFAVLLHAHLAARGIRLRHFRKGKEMKLLAYDDDFDNFQEFQYLKEEQTILPGDNLIT
ECRYNTKDRAEMTWGGLSTRSEMCLSYLLYYPRINLTRCASIPDIMEQLQFIGVKEIYRPVTT
WPFIIKSPKQYKNLSFMDAMNKFKWTKKEGLSFNKLVLVSLPVNVRCSTDNAEWSIQGMTALP
PDIERPYKAEPLVCGTSSSSSLHRDFSINLLVCLLLLSCTLSTKSL

Signal peptide:

amino acids 1-18

Transmembrane domains:

amino acids 56-73, 378-393, 583-602

N-glycosylation sites.

amino acids 114-118, 247-251, 476-480, 517-521

N-myristoylation sites.amino acids 11-17, 15-21, 20-26, 45-51, 68-74, 79-85, 290-296,
316-322, 337-343, 342-348, 456-462, 534-540, 582-588**Copper type II, ascorbate-dependent monooxygenases proteins.**

amino acids 271-321, 422-474

191/550

FIGURE 191

GCTTCAGCTGAAGAAAGAGAGGAATGAAGCGCCTTCTGCTTCTGTTTTTGTTCCTTTATAACAT
TTTCTTCTGCATTTCCCTTAGTCCGGATGACGGAAAATGAAGAAAATATGCAACTGGCTCAGG
CATATCTCAACCAGTTCTACTCTCTTGAAATAGAAGGGAATCATCTTGTTCAAAGCAAGAATA
GGAGTCTCATAGATGACAAAATTCGGGAAATGCAAGCATTTTTTGGATTGACAGTGACTGGAA
AACTGGACTCAAACACCCTTGAGATCATGAAGACACCCAGGTGTGGGGTGCCTGATGTGGGCC
AGTATGGCTACACCCTCCCTGGGTGGAGAAAATACAACCTCACCTACAGAATAATAAACTATA
CTCCGGATATGGCACGAGCTGCTGTGGATGAGGCTATCCAAGAAGGTTTAGAAGTGTGGAGCA
AAGTCACTCCACTAAAATTCACCAAGATTTCAAAGGGGATTGCAGACATCATGATTGCCTTTA
GGACTCGAGTCCATGGTCGGTGTCTCGCTATTTTGATGGTCCCTTGGGAGTGCCTTGGCCATG
CCTTTCCTCCTGGTCCGGGTCTGGGTGGTGACACTCATTTTGATGAGGATGAAAACCTGGACCA
AGGATGGAGCAGGATTCAACTTGTTTCTTGTGGCTGCTCATGAATTTGGTCATGCACTGGGGC
TCTCTCACTCCAATGATCAAACAGCCTTGATGTTCCCAAATTATGTCTCCCTGGATCCCAGAA
AATACCCACTTTCTCAGGATGATATCAATGGAATCCAGTCCATCTATGGAGGTCTGCCTAAGG
TACCTGCTAAGCCAAAGGAACCCACTATACCCCATGCCTGTGACCCTGACTTGACTTTTGAGC
CTATCACAACTTTCCGCAGAGAAGTAATGTTCTTTAAAGGCAGGCACCTATGGAGGATCTATT
ATGATATCACGGATGTTGAGTTTGAATTAATTGCTTCATTCTGGCCATCTCTGCCAGCTGATC
TGCAAGCTGCATACGAGAACCCAGAGATAAGATTCTGGTTTTTAAAGATGAAAACCTCTGGA
TGATCAGAGGATATGCTGTCTTGCCAGATTATCCCAAATCCATCCATACATTAGGTTTTCCAG
GACGTGTGAAGAAAATAGATGCAGCCGTCTGTGATAAGACCACAAGAAAACCTACTTCTTTG
TGGGCATTTGGTGCTGGAGGTTTGATGAAATGACCCAAACCATGGACAAAGGATTCCCGCAGA
GAGTGGTAAAACACTTTCCTGGAATCAGTATCCGTGTTGATGCTGCTTTCAGTACAAAGGAT
TCTTCTTTTTTCAGCCGTGGATCAAAGCAATTTGAATACAACATTAAGACAAAGAATATTACCC
GAATCATGAGAACTAATACTTGGTTTCAATGCAAAGAACCAGAACTCCTCATTGTTTGTG
ATATCAACAAGGAAAAAGCACATTCAGGAGGCATAAAGATATTGTATCATAAGAGTTTAAGCT
TGTTTATTTTTGGTATTGTTCAATTTGCTGAAAAACACTTCTATTTATCAATTAAATTCATAGAC
CTAAAATAAACCTCAACAGGTCTTTTAATATAAATTCTGCTTCAAATAGAATAAAACCATTC
TTTAAACAAC

192/550

FIGURE 192

MKRLLLFLFFITFSSAFPLVRMTENEENMQLAQAYLNQFYSLIEGNHLVQSKNRS LIDDKI
REMQAFFGLTVTGKLDSENTLEIMKTPRCGVPDVGQYGYTLPGWRKYNLT YRIINYTPDMARAA
VDEAIQEGLEVWSKVTP LKFTKISKGIADIMIAFRTRVHGRCPRYFDGPLGVLGHA FPPGPGL
GGDTHFDEDENWTKDGAGFN LFLVAAHEFGHALGLSHSNDQTALMFFNYVSLDPRKYPLSQDD
INGIQSIYGG LPKVPAKPKEPTIPHACDPDLTFDAITTFRRVMMFFKGRHLWRIYYDITDVEF
ELIASFWPSLPADLQAAYENPRDKILVEK DENFWMIRGYAVLPDYPKSIHTLGFPGRVKKIDA
AVCDKTRKTYFFVGIWCWRFD EMTQTMKGFPQRVVKHFPGISIRVDAA FQYKGFFFSRGS
KQFEYNIKTKNITRIMRTNTWFQCKE PKNSSFGFDINKEKAHSGGIKILYHKSLSLFI FGIHV
LLKNTSIYQ

Signal peptide:

amino acids 1-17

N-glycosylation sites.

amino acids 55-59, 110-114, 200-204, 452-456, 470-474, 508-512

N-myristoylation site.

amino acids 71-77, 205-211, 223-229

Hemopexin domain signature.

amino acids 171-202, 207-238, 318-334

Neutral zinc metallopeptidases, zinc-binding region signature.

amino acids 213-223

Matrixins cysteine switch.

amino acids 89-97, 207-238

193/550

FIGURE 193

CACAATCAGGTCCCATTCTATAGATGGGGAAACTGAGGCTTGAGGTCACATAGGCGTCGTTCA
AGGCTGGTATACCTGCACCCTCTCCCATGTGAACAACATGGTTCTGGGTAATGGGGGCTGTCA
TCCAGTCTCCTCCCTGCCCCCTGCTGGTGCACCTTCCTGCCTCTGCTGGTGCACCTTTCTGCCCCCT
ACTGGTATATTTGCTGCCTCTGCTGGGGCGCTTCCTGCCTCGGCTGGTGTATCTCCTGCCCCCT
GCTGGTGCACCTTTCTGCCCCCGCTGATGCACCTTCCTGCCTCTGCTGGTGCACCTTCCTGGCTCT
GCTGGCACACTTCCTGCCTCTGCTGGTGCACCTTCCTGGCTCTGCTGGCGCACTTTCCTGCCCC
TGCTGGTGTATTTCTGCCCCCTGCTGGTGTACTTCCTTCCCCTGCTGGTGCACCTTCCTGCCTC
TGCTGGCGCACTTCTTGCCCTCTCCAGGCCCTACCTTAGCCTCTCCCTCTTATATATGGAAGTCT
TCCCAGTTCACCTGACACTGGTAACAGGGACTCTGCTCTTGGTGTTGCTGTCTGCCCTGGGGAT
GGGCATCTGTGTCTTCCTTTACTACTGCTGGCTCAGGACCCAGAGCTTTGAAGCATGTCCAGA
TGCAGGTCCGGGCACCAGAGTCTAAGGAGCCCCCTACACCCACCAGGATTTTCCAATAAAGAGA
TGTTCACCA

194/550

FIGURE 194

MVLGNGGCHPVSSLPLLVHFLPLLVHFLPLLVYLLPLLGRFLPRLVYLLPLLVHFLPPLMHFL
PLLVHFLALLAHFLPLLVHFLALLAHFPAPAGVFPAPAGVLPSFAGALPASAGALLASPGPT

Signal peptide:

amino acids 1-39

N-myristoylation sites.

amino acids 4-10, 109-115, 116-122

Leucine zipper pattern.

amino acids 14-36, 16-38, 17-39, 21-43, 24-46, 28-50, 31-53,
35-57, 38-60, 42-64, 45-67, 49-71, 52-74, 56-78, 59-81, 63-85,
65-87, 66-88

195/550

FIGURE 195

GGCAAGGCGGGCGGGCGGGCGGGCGGGCAGCCGCGGTGGCGGGCTGGGGAACATCTCGGCAGCCA
CCGCGCTTCTCCCGCTGGAGCGGGCGTCCAGCTTGGCTGCCCTCGGTCCCTGCCACGTT
TCGGGTGCGCCCTGCACCCCCACCCAGGCTCGCTTCTCTTCGAAGCGGGAAGGGCGCCTTGCA
GGATCCTGCCGCCCCCTCCAACCGGATCCTGGGTCTAGAGCTCCCCAGAGCGAGGCGCTCGCCA
GGACTCCTGCCCGCCCAACCCTGACCGCGGGGGGTGCCCCGGGACGTAGCGCCGCGGAGAG
GAAGCGGCAAAGGGGGACCATGCGGGCGCCTGACTCGTCGGCTGGTTCTGCCAGTCTTCGGGGTG
CTCTGGATCACGGTGCTGCTGTTCTTCTGGGTAACCAAGAGGAAGTTGGAGGTGCCGACGGGA
CCTGAAGTGCAGACCCCTAAGCCTTCGGACGCTGACTGGGACGACCTGTGGGACCAGTTTGAT
GAGCGGCGGTATCTGAATGCCAAAAAGTGGCGCGTTGGTGACGACCCCTATAAGCTGTATGCT
TTCAACCAGCGGGAGAGTGAGCGGATCTCCAGCAATCGGGCCATCCCGGACACTCGCCATCTG
AGATGCACACTGCTGGTGTATTGCACGGACCTTCCACCCACTAGCATCATCATCACCTTCCAC
AACGAGGCCCCGCTCCACGCTGCTCAGGACCATCCGCAGTGTATTAAACCGCACCCCTACGCAT
CTGATCCGGGAAATCATATTAGTGGATGACTTCAGCAATGACCCTGATGACTGTAAACAGCTC
ATCAAGTTGCCCAAGGTGAAATGCTTGCGCAATAATGAACGGCAAGGTCTGGTCCGGTCCCGG
ATTCCGGGCGCTGACATCGCCCAGGGCACCCTCTGACTTTCCTCGACAGCCACTGTGAGGTG
AACAGGGACTGGCTCCAGCCTCTGTTGCACAGGGTCAAAGAGGACTACACGCGGGTGGTGTGC
CCTGTGATCGATATCATTAACCTGGACACCTTCACCTACATCGAGTCTGCCTCGGAGCTCAGA
GGGGGGTTTGA CTGGAGCCTCCACTTCCAGTGGGAGCAGCTCTCCCCAGAGCAGAAGGCTCGG
CGCCTGGACCCACGGAGCCCATCAGGACTCCTATCATAGCTGGAGGGCTCTTCGTGATCGAC
AAAGCTTGSTTTGATTACCTGGGGAAATATGATATGGACATGGACATCTGGGGTGGGGAGAAC
TTTGAAATCTCCTTCCGAGTGTGGATGTGCGGGGGCAGCCTAGAGATCGTCCCCTGCAGCCGA
GTGGGGCAGCTCTTCCGGAAGAAGCACCCCTACGTTTTCCTGATGGAAATGCCAACACGTAT
ATAAAGAACACCAAGCGGACAGCTGAAGTGTGGATGGATGAATACAAGCAATACTATTACGCT
GCCCGGCCATTCCGCCCTGGAGAGGCCCTTCGGGAATGTTGAGAGCAGATTGGACCTGAGGAAG
AATCTGCGCTGCCAGAGCTTCAAGTGGTACCTGGAGAATATCTACCCTGAACTCAGCATCCCC
AAGGAGTCCCTCCATCCAGAAGGGCAATATCCGACAGAGACAGAAGTGCTGGAATCTCAAAGG
CAGAACAACCAAGAAACCCCAAACCTAAAGTTGAGCCCCTGTGCCAAGGTCAAAGGCGAAGAT
GCAAAGTCCCAGGTATGGGCCTTCACATACACCCAGCAGATCCTCCAGGAGGAGCTGTGCCTG
TCAGTCATCACCTTGTTCCCTGGCGCCCCAGTGGTTCTTGTCCTTTGCAAGAATGGAGATGAC
CGACAGCAATGGACCAAACTGGTTCCACATCGAGCACATAGCATCCCACCTCTGCCTCGAT
ACAGATATGTTCCGGTATGGCACCGAGAACGGCAAGGAAATCGTCGTCAACCCATGTGAGTCC
TCACTCATGAGCCAGCACTGGGACATGGTGAGCTCTTGAGGACCCCTGCCAGAAGCAGCAAGG
GCCATGGGGTGGTGCTTCCCTGGACCAGAACAGACTGGAACTGGGCAGCAAGCAGCCTGCAA
CCACCTCAGACATCCTGGACTGGGAGGTGGAGGCAGAGCCCCCAGGACAGGAGCAACTGTCT
CAGGGAGGACAGAGGAAAACATCACAAGCCAATGGGCTCAAAGACAAATCCBCATGTTCTCA
AGGCCGTTAAGTTCCAGTCTTGGCCAGTCATTCCCTGATTGGTATCTGGAGACAGAAACCTAA
TGGGAAGTGTTTATTGTTCTTTTCCCTACAAAGGAAGCAGTCTCTGGAGGCCAGAAAGAAAAG
CCTTCTTTTTTCACTAGGCCAGGACTACATTGAGAGATGAAGAATGGAGGTGTTTCCAAAAGA
AATAAAGAGAAACTTAGAAGTTGTCTCTGGAAAAA AAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAA

196/550

FIGURE 196

MRRLTRRLVLPVFGVLWITVLLFFWVTKRKLEVPTGPEVQTPKPSDADWDDLWDQFDERRYLN
AKKWRVGGDPYKLYAFNQRESERISSNRAIPDTRHLRCTLVYCTDLPPTSIIITFHNEARST
LLRTIRSVLNRTPTHIREIILVDDFSDNDPDDCKQLIKLPKVKCLRNNERQGLVRSRIRGADI
AQGTTLTFLDSHCEVNRDWLQPLLHRVKEDYTRVVCPVIDIINLDTFTYIESASELRGGFDWS
LHFQWEQLSPEQKARRLDPTTEPIRTPIIAGGLEVIDKAWFDYLGKYDMDMDIWGGENFEISFR
VWMCGGSLEIVPCSRVGHVERKKHPYVFPDGNANTYIKNTKRTAEVWMDEYKQYYAARPFAL
ERFPGNVESRLDLRKNLRCQSFKWYLENIYPELSIPKESSIQKGNIRQRQKCLESQRQNNQET
PNLKLSPCAKVKGEDAKSQVWAFTYTQQILQEELCLSVITLFPGAPVVLVLCKNGDDRQQWTK
TGSHEHIAHSLCLDTDMFGDGTENGKEIVVNPCESSLMSQHWDMVSS

Transmembrane domain:

amino acids 475-493

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 2-6

Tyrosine kinase phosphorylation sites.

amino acids 68-75, 401-409

N-myristoylation sites.

amino acids 178-184, 186-192, 192-198, 346-352, 383-389, 526-532

197/550

FIGURE 197

GCAGCTCACCCTTCGCGAGCCGCGATGGGGGAAGACGACGCCGCGCTTCGGGCTGGCAGCAGGGGGCTCTCCGACC
 CGTGGGCAGACTCAGTGGGAGTGCAGACCCCGCACACGAGCGCCACATCGCCGTACACAAGCGGCTTGTGCTGG
 CCTTCGCTGTGTCCCTCGTGGCATTTGCTCGCGGTCACAATGCTCGCTGTGCTCAGCCTGCGCTTCGACGAGT
 GCGGGGCGAGTGCCACGCCAGGCGCGGACGGTGGCCCCCTCAGGCTTTCGGAGCGCGGCGGCAACGGGAGCCTCC
 CTGGATCGGCCCCGGCGCAACCACCGCAGGCGGGGACTCCTGGCAGCCCCAGGCGGGTGGGGTGGCCAGTCCGG
 GGACCACGTCCGCCAGCCGCCGTGCGAGGAGGAGCGGGAGCCGTGGGAGCCGTGGACGCAGCTGCGCCTGTCCG
 GCCACCTGAAGCCGCTGCACTACAATCTGATGCTCACCBCCTTCATGGAGAATTCACCTTCTCCGGGGAGGTCA
 ACGTGGAGATCGCGTSCCGGAACGCCACCCGCTACGTAGTGTGTCACGCTTCCCGAGTGGCGGTGGAGAAAGTGC
 AGCTGGCCGAGGACCGGGCGTTCCGGGCTGTCCCTGTAGCCGCTTTTTCCTCTACCCGCAACCCAGGTCTTAG
 TGGTGGTGTGTAATAGGACACTGGACGCGCAGAGGAATTACAATCTGAAGATTATCTACAACGCGCTCATCGAGA
 ATGAGCTCCTGGGCTTCTTCCGCGAGCTCCTATGTGCTCCACGGGGAGAGAAAGATTCCCTTGGTGTACTCAGTTTT
 CGCCTACACATGCCAGAAAGGCATTTCTTGTTTTGTATGAGCCAATCTACAAGGCTACTTTCAAATCAGCATCA
 AGCATCAAGCAACCTATTTATCTTTATCTAATATGCCAGTGGAACTTCCGTGTTTGAGGAAGATGGATGGGTTA
 CGGATCACTTTTACAGACCCCTCTCATGTCCACATATTATTTAGCCTGGGCAATTTGCAACTTCACATACAGAG
 AAACCTACCACCAAGAGTGGGCTTGTAGTACGATTATATGCAAGACCTGATGCTATCAGAAGAGGATCCGGGGACT
 ATGCTCTCCATATAACAAAGAGATTAATAGAATTTTATGAAGACTACTTTAAAGTGGCCTATTCCTTGGCAAAAC
 TAGATCTTTTAGCTGTGCCAAGCATCCGTATGCTGCTATGGAGAAGTGGGACTAAGTATTTTGTGGAAACAA
 GAATAGTCTGGATCCCAGTGTTCATCTATTTCTTATTTGCTGGATGTCACCATGGTTCATGGTTCATGAGATAT
 GTCACCAAGTGGTTTGGTGACCTTGTGACGCTGTGTGGTGGGGAAGACGTGTGGCTGAAGGAAGGGTTTGTCTACT
 ACTTTGAATTTTGTGGTACAGACTACCTCTATCCTGGCTGGAACATGGAAAAGCAGAGGTTTCTGACCGATGTTC
 TGCATGAAGTGATGCTGCTGGACGGTTTGGCCAGTTCCTATCCAGTATCACAGGAAGTGTGTCAGGCAACAGATA
 TTGACAGGGTGTGTTGACTGGATCGCATATAAAAAGGGTGTGCTTTAATAAGAATGCTGGCTAATTTTATGGGCC
 ATTCAGTTTTCAGAGGGGTTTGAAGATTATTTAACCATTCTAAGTATGGTAATGCAGCCAGAAATGATCTCT
 GGAATACATTATCGGAGGCTTTAAAAAGAAATGGGAAATATGTAATATACAAGAAGTAATGGATCAGTGGACAC
 TCCAGATGGGTTATCCTGTTATCACCATCTTGGGAAACACAACAGCAGAGAAATAGAATAATAATTACCAACAGC
 ATTTTATCTATGATATCAGTGTCTAAACTAAGCACTTAAACTTCAGAAATACAGTTACCTGTGGCAGATTCCAT
 TAACATTTGTGGTAGGAAATAGAAGCCATGTGCTTTCAGAAAGCAATTTTGGGTGTCTAACAAATCAGAGCACC
 ACAGAACTAATTTTGGACAAAGGAAGCTGGCTGCTGGCGAACATCAATCAAACCTGGCTATTTTAGAGTCAACT
 ATGACCTAAGGAACCTGGAGATTATTAATTGATCAATTAATCCGGAATCATGAGGTTCTTTCTGTCTAGTAACCGAG
 CGGGCTTGATCGATGATGCCTTCAGCCTAGCCAGGGCTGGCTATTTGCCTCAGAAATATTCCTCTGGAGATTATCA
 GATACCTGTCTGAGGAGAAGGATTTTCTTCTTGGCATGCTGCCAGCCGAGCTCTTTATCCTCTAGATAAATTAC
 TGGACCGCATGGAAAACCTACAACATTTTCAATGAATATATTTTAAAGCAAGTTGCAACAACATATATCAAGCTTG
 GGTGGCCGAAAAATAATTTTAAATGGATCTCTTGTTCAGCATCCTACCAACATGAAGAACTACGTAGAGAAGTTA
 TAATGCTGGCCTGCASTTTTGGCAACAAGCATGTCACCAACAGGCATCAACACTTATTTAGATTGGATTTCCTCA
 CAACAGGAACAGAAATACCATAAATGTTAGAGACTCCTATACCTGTACAGGAGTGTCACTACTGGATGAGGATG
 TCTGGGAATTCATATGGATGAATTTCCATTCCACCACAGCAGTTTCTGAGAAGAAATATTTATTGGAAGCCTTAA
 CTTGCAGTGATGACAGGAATTTATTAACAGGCTTCTAAATCTGTCACTGAATTTCTGAGGTGGTGTGATCAAG
 ATGCAATTTGATGTCAATCCATGTAGCTCGAAATCCACATGGTTCGAGACCTTGCCTGGAAGTTTTTTCAGGGATA
 AATGGAAGATATTAATACCAGGTATGGAGAAGCATTGTTTATGTATTCCAAACCTCATCAGTGGTGTACAGAAAT
 TTCTTAATACTGAAGGTGAACCTCAAAGAGCTCAAGAACTTCATGAAAACTATGATGGGGTAGCTGCTGCTTCTT
 TCTCAGAGCTGTGGAACTGTGGAAGCCAATGTGCGCTGGAAAATGCTTTACCAAGACGAGCTTTTCCAATGGT
 TAGGAAAAGCTCTAAGACACTAATATATGATCTTATAAAACAAACAACTCAACTCAGAAGTTTATGAGAAGACAC
 GCTTTTTTGTGGAATGAGGAAAATGTACTACCTAGAAAATGGCCAGATTTTCACTGTTAACGTGTGGGAGGAATTT
 TTTTTTTTGTGTTTTTATTTTTTGGTTTTGGGGGATATTTTTTATTTGTTTCATTCATTCGTCTGTTTTCTCTAC
 TGGGTGTTCTCTCTAAAGAACTCTTGCAAGTGAAACTAGCCATGATTGCTTCAGCTGTACATTCCTTGTCTGTA
 CAGGACCAATATGATAGTGATGCATGTTGATGTTACAGTCAATTTGGAAAAACATATTCAGAATATCTGTGCAT
 GGATATATTGTCCTGCCTGTGTTCCAGCATGCTTATTTCAAACGTCCAGTGTGTTGTGTGTAATATGTGTTACACC
 TAGGATGGGCATTATGCAAAAGCACAAAGATTATATATGACAATCAGTATTGCAATGAAAGAAAACTAAAAACA
 GAAATGATATTCTCAATTTTGGGCAATGTGAGAGGTAAAATAGCCCTTGACATGATGAACATCACTTATTTTCAGC
 ACTTGGATTGTCTGGCAATGATTACTGTGTTGCTAACTCATTTTCTTTGAGTTAAAGCTGTGTATACATTTTAA
 AGGCATATAGATAGTGTATGCATATGTATATGTACATAGGGAAGCCCCATATGTATATAGTATGTTGTACACTGC
 ACATGTACAAAGAATGTCTTCAGATCAAAGAAAATTTATCTCTTTTATAAACTTAAGGACAGTTGCAAAAGGCT
 TCAAGGAATTTATCTCAACATTATTTCTTCTATGCTCTAAATTTCTCAACTGTTATGAATTTTTTCATCTAC
 TTCTTGAACAGTGGTCTATTCTGCTACATGAAGATGAATACAAACAAAATTTTTGTATAAACTCCCCAAAAA
 AAAAAA

198/550

FIGURE 198

MGEDDAALRAGSRGLSDPWADSVGVRPRPTTERHIAVHKRLVLAFVSLVALLAVTMLAVLLSL
 RFDECGASATPGADGGPSGFPERGGNGSLPGSARRNHAGGDSWQPEAGGVASPGTTSAQPPS
 EEEREPWEPWTQLRLSGHLKPLHYNLMLTAFMENFTFSGEVNVVEIACRNATRYVVLHASRVAV
 EKVQLAEDRAFGAVPVAGFFLYPQTQVLVVVLNRTLDAQRNYNLKI IYNALIENELLGFFRSS
 YVLHGERRFLGVTQFSPTHARKAFPCFDEPIYKATFKISIKHQATYLSLSNMPVETSVFEEDG
 WVTDFHSQTPLMSTYYLAWAICNFTYRETTTKSGVVVRLYARPDARRGSGDYALHITKRLIE
 FYEDYFKVPYSLPKDLLAVPKHPYAAMENWGLSIFVEQRILLDFSVSSISYLLDVTMVIVHE
 ICHQWFGDLVTPVWWEDVWLKEGFAHYFEFVGTDYLYPGWNMEKQRFLLDVLHEVMLLDGLAS
 SHPVSQEVQLQATDIDRVFDWIAYKKGAALIRMLANFMGHSVFQRLQDYLTIHKYGNAARNDL
 WNTLSEALKRNGKYVNIQEVMDQWTLQMGYPVITILGNTTAENRIIITQQHFIYDISAKTKAL
 KLQNNSYLWQIPLTIVVGNRSHVSSEAIWVSNKSEHHRITYLDKGSWLLGNINQTYFRVNY
 DLRNWRLLIDQLIRNHEVLSVSNRAGLIDDAFSLARAGYLPQNIPLEIIRYLSEEKDFLPWHA
 ASRALYPLDKLLDRMENYNIFNEYILKQVATTYIKLGWPKNNFNGSLVQASYQHEELRREVIM
 LACSGFNKHCHQQASTLISDWISSNRNRIPLNVRDIVYCTGVSLLEDVWEEFIWMKFHSTTAV
 SEKKILLEALTCSDDRNLLNRLNLSLSEVVLDQDAIDVIIHVARNPHGRDLAWKFFRDKWK
 ILNTRYGEALFMYSKLISGVTEFLNTEGELKELKNFMKNYDGVAAASFRAVETVEANVRWKM
 LYQDELFPQWLKGKALRH

Transmembrane domain:

amino acids 44-63

N-glycosylation sites.

amino acids 89-93, 160-164, 175-179, 222-226, 338-342, 605-609,
 634-638, 649-653, 663-667, 684-688, 800-804, 906-910

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 362-366

Tyrosine kinase phosphorylation site.

amino acids 520-528

N-myristoylation sites.

amino acids 78-84, 87-93, 90-96, 118-124, 501-507, 604-610,
 825-831, 987-993

Neutral zinc metalloproteinases, zinc-binding region signature.

amino acids 437-447

199/550

FIGURE 199

GCGCCCGGCGCAGCTCGGCCAGAGCGACCGCGGGGCTGAGCGCGCGTCCGCCAGGGGGCTCCGGAAGCTGCCCC
 GGCCCGCGGCTCCTCCCTCGCTCCCGCTTCCCTTTCTCGCTCACCSCCGCCCTCCTTCCCCAGCTCCCTCGCC
 GTCCGCCCGCCCCACAGCCAGCGGCTCCGCGCCCCCTGCAGCCACGATGCCCCGCGGCCCGGCCCGCCGCGGG
 ACTCCGCGGGATCTCGCTGTTCTCGCTCTGCTCCTGGGAGCCCCGGCGGCAGCGCTGGAGCGAGATGCTCTTCC
 CGAGGGAGATGCTAGCCCTTTGGGTCTTACCTCCTGCCCTCAGGAGCCCCGGAGAGAGGCAGTCTCTGGCAAAGA
 GCACCCTGAAGAGAGAGTGGTAACAGCGCCCCCAGTTCCCTCACAGTCGGCGGAAGTGCTGGGCGAGCTGGTGCT
 GGATGGGACCGCACCTCTGCACATCACGACATCCCAGCCCTGTCACCGCTGCTTCCAGAGGAGGCCCGCCCCAA
 GCACGCCCTTGCCCCCAAGAAGAACTGCCTTCGCTCAAGCAGGTGAACCTCGCCAGGAAGCAGCTGAGGCCCAA
 GGCCACCTCCGCAGCCACTGTCCAAAGGGCAGGGTCCCAGCCAGCGTCCCAGGGCCTAGATCTCCTCTCCTCCTC
 CACGGAGAAGCCTGGCCACCGGGGGACCCGGACCCCATCGTGGCCCTCCGAGGAGGCATCAGAAGTGCCCTTTG
 GCTGGATCGAAAGGAGAGTGGGTCCCTACAACACCCGACCCCTGCAAAATCTCCCCCTTCACTTCGCAGCCCTA
 TGTGGCCACACACTCCCCAGAGGCCAGAACCCGGGGAGCCTGGGCCTGACATGGCCCAGGAGGCCCCCCAGGA
 GGACACCAGCCCCATGGCCCTGATGGACAAAGGTGAGAATGAGCTGACTGGGTGAGCCTCAGAGGAGAGCCAGGA
 GACCACTACCTCCACCATTATCACCACCACGGTCATCACCACCGAGCAAGCACCAGCTCTCTGCAGTGTGAGCTT
 CTCCAATCCTGAGGGGTACATTGACTCCAGCGACTACCCACTGCTGCCCTTCAACAACTTTCTGGAGTGCACATA
 CAACGTGACAGTCTACACTGGCTATGGGGTGGAGCTCCAGGTGAAGAGTGTGAACCTGTCCGATGGGGAAGTGT
 CTCCATCCGCGGGGTGGACGGCCCTACCCTGACCGTCTTGGCCAACCAGACACTCCTGGTGGAGGGGCAGGTAAT
 CCGAAGCCCCACCAACACCATCTCCGTCTACTTCCGGACCTTCCAGGACGACGGCCTTGGGACCTTCCAGCTTCA
 CTACCAGGCCTTCATGCTGAGCTGCAACTTTCCCCCGCCGGCCTGACTCTGGGGATGTACGCTGATGGACCTGCA
 CTCAGGTGGGGTGGCCCACTTTCACTGCCACCTGGGCTATGAGCTCCAGGGCGCTAAGATGCTGACATGCATCAA
 TGCCTCCAAGCCGCACTGGAGCAGCCAGGAGCCCATCTGCTCAGCTCCTTGTGGAGGGGCAGTGCACAATGCCAC
 CATCGGCCCGCTCCTCTCCCCAAGTTACCTGAAAACACAAATGGGAGCCAAITTCGATCTGGACGATTGAAGC
 TCCAGAGGGCCAGAAGCTGCACCTGCACCTTGGAGAGGCTGTTGCTGCATGACAAGGACAGGATGACGGTTACAG
 CGGGCAGACCAACAAGTCAGCTCTTCTTACGACTCCCTTCAAACCGAGAGTGTCCCTTTTGGAGGGCCTGCTGAG
 CGAAGGCAACACCATCCGCATCGAGTTCACGTCCGACAGGCGCCGGCGGCCCTCCACCTTCAACATCCGATTTGA
 AGCGTTTGAGAAAGGCCACTGCTATGAGCCCTACATCCAGAATGGGAACCTCACTACATCCGACCCGACCTATAA
 CATTTGGGACTATAGTGGAGTTCACCTGGGACCCCGGCCACTCCCTGGAGCAGGGGCCCGGCCATCATCGAATGCAT
 CAATGTGCGGGACCCATACTGGAATGACACAGAGCCCTGTGCAGAGCCATGTGTGGTGGGGAGCTCTCTGCTGT
 GGCTGGGGTGTATTGTCCCCAACTGGCCCCGAGCCCTACGTGGAAGGTGAAGATTGTATCTGGAAGATCCACGT
 GGGAGAAGAGAAACGGATCTTCTTAGATATCCAGTTCCTGAATCTGAGCAACAGTGACATCTTGACCATCTACGA
 TGGCGACGAGGTTCATGCCCCACATCTTGGGGCAGTACCTTGGGAACAGTGGCCCCCAGAACTGTACTCCTCCAC
 GCCAGACTTAACCATCCAGTTCATTTCGGACCCCTGCTGGCCTCATCTTTGGAAAGGGCCAGGGATTTATCATGAA
 CTACATAGAGGTATCAAGGAATGACTCCTGCTCGGATTTACCCGAGATCCAGAATGGCTGGAAACCACTTCTCA
 CACGGAGTTGGTGCGGGGAGCCAGAATCACCTACCACTGTGACCCCGGCTATGACATCGTGGGGAGTGACACCT
 CACCTGCCAGTGGGACCTCAGCTGGAGCAGCGACCCCATTTTGTGAGAAAATTATGTACTGCACCGACCCCGG
 AGAGGTGGATCACTCGACCCGCTTAATTTCCGATCCTGTGCTGCTGGTGGGGACCAACATCCAATACACCTGCAA
 CCCCCTTTTGTGCTTGAAGGGAGTTCTCTTCTGACCTGCTACAGCCGTGAAACAGGGACTCCCATCTGGACGTC
 TCGCCTGCCCACTGCGTTTCGGAGGAGTCCCTGGCATGTGACAACCCAGGGCTGCCGAAATGGATACCAAT
 CCTGTACAAGCGACTCTACCTGCCAGGAGAGTCCCTCACCTTCATGTGCTACGAAGGCTTTGAGCTCATGGGTGA
 AGTGACCATCCGCTGCATCCTGGGACAGCCATCCCACTGGAACGGGCCCTGCCCGTGTGTAAAGTTAATCAAGA
 CAGTTTTGAACATGCTTTAGAAGCAGAAGCGGCAGCAGAGACGTGCTGGAAGGGGGGAACATGGCCCTGGCTAT
 CTTATCCCGGTCTCATCATCTCCTTACTGCTGGGAGGAGCCTACATTTACATCACAAGATGTGCTACTATTCT
 CAACCTCCGCTGCTCTGATGTACTCCACCCCTACAGCCAGATCACCGTGGAAACCGAGTTTGACAACCCCAT
 TTACGAGACAGGGGAAACAGAGAGTATGAGTTTCTATCTAAGAGAGCTACACTTGAGAAGGGGACTTTGTGAA
 CTCACACCACAATCTCCTCGAGACATTATCCAGAGACCATGTGGCACTTGGATTGAAACCCAGAAATGTCGACTGT
 CTTTTGTTAGACTCTTTATCAAAGGTTTACTGTTTTCTTCCCTGTATTTATTATATTTAAAAGTGAAAAAAA
 AAAAAAAA

200/550

FIGURE 200

MPAARPPAAGLRGISLFLALLLGSPAAALERDALPEGDASPLGPYLLPSGAPERGSPGKEHPE
 ERVVTAPPSSSSQSAEVLGELVLDGTAPSAHHDIPALSPLLPEEARPKHALPPKKKLPSLKQVN
 SARKQLRPKATSAATVQRAGSQPASQGLDLLSSSTEKPGPPGDPDPIVASEEASEVPLWLDRK
 ESAVPTTPAPLQISPFTSQPYVAHTLPQRPEPGEPGPDMAQEAPQEDTSPMALMDKGENELTG
 SASEESQETTTSTIITTTVITTEQAPALCSVSFSNPEGYIDSSDYPLLPLNPFLECTYNVTY
 TGYGVELQVKS VNLS DGELLSIRGVDGPTLTVLANQTLLVEGQVIRSPTNTISVYFRTFQDDG
 LGTFQLHYQAFMLSCNFPRRPDSGDVTVMDLHSGGVAHFHCHLGYELQGAKMLTCINASKPHW
 SSQEPICSAPCGGAVHNATIGRVLSPSY PENTNGSQFCIWTIEAPEGQKLHLHFERLLLHDKD
 RMTVHSGQTNKSALLYDSLQTESVPFEGLLSEGNTIRIEFTSDQARAASTFNIRFEAFEKGHC
 YEPYIQNGNFTTSDPTYNIGTIVEFTCDPGHSLEQGPALIECINVRDPYWNDTEPLCRAMCGG
 ELSAVAGVVLSPNWPEPYVEGEDCIWKIHVGEEKRIFLDIQFLNLSNSDILTIYDGDEVMPHI
 LGQYLGNSGPQKLYSSTPDLTIQFHS DPAGLIFGKGQGFIMNYIEVSRNDSCSDLPEIQNGWK
 TTSHTELVRGARITYQCDPGYDIVGSDTLTCQWDLSSWSDPPFCEKIMYCTDPGEVDHSTRLI
 SDPVLVGTTIQYTCNPGFVLEGSSLLTCYSRETGTPIWTSRLPHCVSEESLACDNPGLPENG
 YQILYKRLYLPGESLTFMCEYEGFELMGEVTIRCILGQPSHWNGPLPVCKVNQDSFEHALEAEA
 AAETSLEGGNMALAI FIPVLIISLLLGGAYIYITRCRYYSNLRLPLMYSHPYSQITVETEDN-
 PIYETGETREYEVSI

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 893-915

N-glycosylation sites.

amino acids 311-315, 328-332, 350-354, 435-439, 458-462, 474-478,
 514-518, 576-580, 618-622, 674-678, 742-746

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 188-192

N-myristoylation sites.

amino acids 23-29, 87-93, 146-152, 454-460, 475-481, 575-581,
 629-635, 695-701, 723-729, 766-772, 877-883, 953-959

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 383-394

201/550

FIGURE 201

GATGGCTACGGCAGGGGGTGGCTCTGGGGCTGACCCGGGAAGTCGGGGTCTCCTTCGCCTTCT
GTCTTTCTGCGTCCTACTAGCAGGTTTGTGCAGGGGAACTCAGTGGAGAGGAAGATATATAT
CCCCTTAAATAAAACAGCTCCCTGTGTTGCGCTGCTCAACGCCACTCATCAGATTGGCTGCCA
GTCTTCAATTAGTGGAGACACAGGGGTATCCACGTAGTAGAGAAAGAGGAGGACCTACAGTG
GGTATTGACTGATGGCCCCAACCCCCCTTACATGGTTCTGCTGGAGAGCAAGCATTTTACCAG
GGATTTAATGGAGAAGCTGAAAGGGAGAACCAGCCGAATTGCTGGTCTTGCAGTGTCTTGGAC
CAAGCCAGTCTCTGCTCAGGCTTCTCTCCTAGTGTACAGTGCCCAAATGATGGGTTTGGTGT
TTACTCCAATTCTTATGGGCCAGAGTTTGTCTACTGCAGAGAAATACAGTGGAATTCGCTGGG
CAATGGTTTGGCTTATGAAGACTTTAGTTTCCCCATCTTTCTTCTTGAAGATGAAAATGAAAC
CAAAGTCATCAAGCAGTGCTATCAAGATCACAACTGAGTCAGAATGGCTCAGCACCAACCTT
CCCCTATGTGCCATGCAGCTCTTTTACACATGCATGCTGTCATCAGCACTGCCACCTGCAT
GCGGCGCAGCTCCATCCAAAGCACCTTCAGCATCAACCAGAAATCGTCTGTGACCCCCCTGTC
TGATTACAATGTGTGGAGCATGCTAAAGCCTATAAATACAACCTGGGACATTAAAGCCTGACGA
CAGGGTTGTGGTTGCTGCCACCCGGCTGGATAGTCGTTCTTTTCTGGAATGTGGCCCCAGG
GGCTGAAAGCGCAGTGGCTTCTTTGTCAACCAGCTGGCTGCTGCTGAAGCTTTGCAAAGGC
ACCTGATGTGACCACCCTGCCCCGCAATGTCATGTTTCTCTTTCAAGGGGAACTTTTGA
CTACATTGGCAGCTCGAGGATGGTCTACGATATGGAGAAGGGCAAGTTTCCCGTGCAGTTAGA
GAATGTTGACTCATTTGTGGAGCTGGGACAGGTGGCCTTAAGAACTTCATTAGAGCTTTGGAT
GCACACAGATCCTGTTTCTCAGAAAAATGAGTCTGTACGGAACCAGGTGGAGGATCTCCTGGC
CACATTGGAGAAGAGTGGTGTGCTGGTGTCCCTGCTGTATCCTCAGGAGGCCAAATCAGTCCCA
GCCTCTCCCACCATCTTCCCTGCAGCGATTTCTTCGAGCTCGAAACATCTCTGGCGTTGTTCT
GGCTGACCCTCTGGTGCCTTCCATAACAAATATTACCAGAGTATTTACGACACTGCTGAGAA
CATTAATGTGAGCTATCCCGAATGGCTGAGCCCTGAAGAGGACCTGAACCTTTGTAACAGACAC
TGCCAAGGCCCTGGCAGATGTGGCCACGGTGTGAGGAGCTGCTCTGTATGAGCTTGACAGGAGG
AACCAACTTCAGCGACACAGTTCAGGCTGATCCCCAAACGGTTACCCGCCTGCTCTATGGGTT
CCTGATTAAAGCCAACAACCTCATGGTTCCAGTCTATCCTCAGGACGACCTAAGGTCTTACTT
GGGTGACGGGCCTCTTCAACATTACATCGCTGTCTCCAGCCCCACCAACACCCTTATGTTGT
ACAGTATGCCTTGGCAAATTTGACTGGCACAGTGGTCAACCTCACCCGAGAGCAGTGCCAGGA
TCCAAGTAAAGTCCCAAGTGAACAAGGATCTGTATGAGTACTCATGGGTCCAGGGCCCTTT
GCATTCTAATGAGACGGACCGACTCCCCCGGTGTGTGCGTTCTACTGCACGATTAGCCAGGGC
CTTGCTCCTGCCTTTGAACCTGAGTCAGTGGAGCTCTACTGAATACTCTACATGGACTGAGAG
CCGCTGGAAAGATATCCGTGCCCCGATATTTCTCATCGCCAGCAAAGAGCTTGAGTTGATCAC
CCTGACAGTGGGCTTCGGCATCCTCATCTTCTCCCTCATCGTCACCTACTGCATCAATGCCAA
AGCTGATGTCCTTTTCATTGCTCCCCGGGAGCCAGGAGCTGTGTATAC**TG**AGGAGGACCCCA
GCTTTTCTTGCCAGNTCAGCAGTTCACCTCCTAGAGCATCTGTCCCCTGGGACACAACCACT
AATTTGTCACTGGAACCTCCCTGGGCCTGTCTCAGATTGGGATTAACATAAAAGAGTGGAAC
ATCCAAAAGAGACAGGGAGAAATAAATAAATTGCCTCCCTTCCCTCCGCTCCCCTTTCCCATCA
CCCCTTCCCATTTCCTCTTCCCTTCTCTACTCATGCCAGATTTTGGGATTACAAATAGAAGCT
TCTTGCTCCTGTTTAACTCCCTAGTTACCCACCCTAATTTGCCCTTCAGGACCCTTCTACTTT
TTCCTTCTGCCCCGTACCTCTCTCTGCTCCTCACCCCCACCCCTGTACCCAGCCACCTTCT
GACTGGGAAGGACATAAAAGGTTTAAATGTCAGGGTCAAACCTACATTGAGCCCCTGAGGACAGG
GGCATCTCTGGGCTGAGCCTACTGTCTCCTTCCCACTGTCTTTCTCCAGGGCCCTCAGATGGC
ACATTAGGGTGGGCGTGTGCGGGTGGGTATCCACCTCCAGCCCACAGTGCTCAGTTGTACT
TTTTATTAAGCTGTAATATCTATTTTGTGTTTTGTCTTTTCTTTTCTTTTGTAAATAT
ATATATAATGAGTTTCATTAAATAGATTATCCC

202/550

FIGURE 202

MATAGGGSGADPGSRGLLRLLSFCVLLAGLCRGNSVERKIYIPLNKTAFCVRLLNATHQIGCQ
SSISGDTGVIHVVEKEEDLQWVLTGDPNPPYMVLLLESKHFTTRDLMEKLGKGRTSRIAGLAVSLT
KPSPASGFSPSVQCPNDGFGVYSNSYGPEFAHCREIQWNSLGNGLAYEDEFSPFI FLEDENET
KVIKQCYQDHNLSQNGSAPTFFPLCAMQLFSHMHAVISTATCMRRSSIQSTFSINPEIVCDPLS
DYNVWSMLKPINTTGTLKPDDRNVVAATRLDSRSFFWNVAPGAESAVASFVTQLAAAEALQKA
PDVTTLPRNVMFVFFQGETFDYIGSSRMVYDMEKGKFPVQLENVDSFVELGQVALRTSLELWM
HTDPVSQKNESVRNQVEDLLATLEKSGAGVPAVILRRPNQSQPLPPSSLQRFLRARNISGVVL
ADHSGAFHNKYYQSIYDTAENINVSYPEWLSPEEDLNFTVDTAKALADVATVLGRALYELAGG
TNFSDTVQADPQTVTRLLYGFLIKANNSWFQSILRQDLRSYLGDGPLQHYIAVSSPTNTTYVV
QYALANLTGTVVNLTREQCQDPSKVPSENKDLYEYSWVQGPLHSNETDRLPRCVRSTARLARA
LSPAFELSQWSSTEYSTWTESRWKDIRARIFLIASKELELITLTVGFGILIFSLIVTYCINAK
ADVLFIAPREPGAVSY

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 671-692

N-glycosylation sites.

amino acids 45-49, 55-59, 187-191, 200-204, 204-208, 264-268,
387-391, 417-421, 435-439, 464-468, 506-510, 530-534, 562-566,
573-577, 580-584, 612-616

Glycosaminoglycan attachment site.

amino acids 404-408

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 232-236

N-myristoylation site.

amino acids 5-11, 6-12, 9-15, 29-35, 61-67, 120-126, 146-152,
168-174, 205-211, 294-300, 438-444, 446-452, 504-510, 576-582

203/550

FIGURE 203

GCTAGACCGAGCCCTGGGAGGCTACGGGCTCCCCGGAAACCCCTGCCAGGGGAGCCGGGTTTT
GAGCTCAGGCGCCTCTAGCGGCGGCCCCAGAAATCTGACTCGCGAGGCCAGAGTTGCAGGGA
CTGAATAGCAAACCTGAGGCTGAGTAGGGAACAGACC**ATG**AGGTCACTGCAGATCTTCCTCTCC
CAATGCCGTTTGTCTCTTCTACTAGTTCCGACAATGCTCCTTAAGTCTCTTGGCGAAGATGTA
ATTTTTCACCCTGAAGGGGAGTTTGACTCGTATGAAGTCACCATTCTTGAGAAGCTGAGCTTC
CGGGGAGAGGTTGCAGGGTGTGGTCACTCCCGTGTCTACCTACTGCAGTTAAAAGGCAAGAAG
CACGTCCTCCATTTGTGGCCCAAGAGACTTCTGTTGCCCGACATCTGCGCGTTTTCTCCTTC
ACAGAACATGGGGAACCTGCTGGAGGATCATCCTTACATAACAAAGGACTGCAACTACATGGGC
TCCGTGAAAGAGTCTCTGGACTCTAAAGCTACTATAAGCACATGCATGGGGGGTCTCCGAGGT
GTATTTAACATTGATGCCAAACATTACCAAATTGAGCCCCTCAAGGCCCTCTCCAGTTTTGAA
CATGTCGTCTATCTCCTGAAGAAAGAGCAGTTTGGGAATCAGGTTTGTGGCTTAAGTGATGAT
GAAATAGAATGGCAGATGGCCCCCTTATGAGAATAAGGCGAGGCTAAGGGACTTTCCTGGATCC
TATAAACACCCAAAGTACTTGGAATTGATCCTACTCTTTGATCAAAGTAGGTATAGGTTTTGTG
AACAACAATCTTTCTCAAGTCATACATGATGCCATTCTTTTGACTGGGATTATGGACACCTAC
TTTCAAGATGTTTCGTATGAGGATACACTTAAAGGCTCTTGAAGTATGGACAGATTTTAACAAA
ATACGCGTTGGATATCCAGAGTTAGCTGAAGTTTtaggcagatTTGTAATATATAAAAAAAGT
GTATTAAATGCTCGCCTGTCATCAGATTGGGCACATTTATATCTTCAAAGAAAATATAATGAT
GCTCTTGCAATGGTCGTTTGGAAAAGTGTGTTCTCTAGAATATGCTGGATCAGTGAGTACTTTA
CTAGATACAAATATCCTTGCCCCCTGTACCTGGTCTGCTCATGAGCTGGGTCATGCTGTAGGA
ATGTCACATGATGAACAATACTGCCAATGTAGGGGTAGGCTTAATTGCATCATGGGCTCAGGA
CGCACTGGGTTTAGCAATTGCAGTTATATCTCTTTTTTAAACATATCTCTCGGGAGCAACA
TGTCTAAATAATATCCCAGGACTAGGTTATGTGCTTAAGAGATGTGGAAACAAAATTGTGGAG
GACAATGAGGAATGTGACTGTGGTCCACAGAGGAGTGTGAGAAAGATCGGTGTTGCCAATCA
AATTGTAAGTTGCAACCAGGTGCCAAGTGTAGCATTGGACTTTGCTGTCTATGATTGTCGGTTT
CGTCCATCTGGATACGTGTGTAGGCAGGAAGGAAATGAATGTGACCTTGCAAGTACTGCGAC
GGGAATTCAAGTTCCTGCCCAAATGACGTTTATAAGCAGGATGGAACCCCTTGCAAGTATGAA
GGCCGTTGTTTCAGGAAGGGGTGCAGATCCAGATATATGCAGTGCCAAAGCATTTTTGGACCT
GATGCCATGGAGGCTCCTAGTGAGTGCTATGATGCAGTTAACTTAATAGGTGATCAATTTGGT
AACTGTGAGATTACAGGAATTCGAAATTTTAAAAAGTGTGAAAGTGCAAATTCATATGTGGC
AGGCTACAGTGTATAAATGTTGAAACCATCCCTGATTTGCCAGAGCATACTACTATAATTTCT
ACTCATTTACAGGCAGAAAATCTCATGTGCTGGGGCACAGGCTATCATCTATCCATGAAACCC
ATGGGAATACCTGACCTAGGTATGATAAATGATGGCACCTCCTGTGGAGAAGGCCGGGTATGT
TTTAAAAAAATTGCGTCAATAGCTCAGTCCTGCAGTTTGACTGTTTGCCTGAGAAATGCAAT
ACCCGGGGTGTTTGCAACAACAGAAAAAAGTCCACTGCATGTATGGGTGGGCACCTCCATTC
TGTGAGGAAGTGGGGTATGGAGGAAGCATTGACAGTGGGCCTCCAGGACTGCTCAGAGGGGCG
ATTCCCTCGTCAATTTGGGTGTGTCCATCATAATGTTTCGCCTTATTTTATTAATCCTTTCA
GTGGTTTTTGTGTTTTTCCGGCAAGTGATAGGAAACCACTTAAACCCAAACAGGAAAAAATG
CCACTATCCAAAGCAAAAAGTGAACAGGAAGAATCTAAACAAAAAAGTGTACAGGAAGAATCT
AAAACAAAAAAGTGGACAGGAAGAATCTGAAGCAAAAAGTGGACAGGAAGAATCTAAAGCAAAA
ACTGGACAGGAAGAATCTAAAGCAAACATTGAAAGTAAACGACCCAAAGCAAAGAGTGTCAAG
AAACAAAAAAG**TAA**CCGGGCAATCCATACTCATTCAGTAACACAGGCTCATTATTTAACCA
GCTAATCATTTATCCAAAGGCTTTCCATTCTTCTCCAATATTTTTTTTACTTTAATTTTTCCC
ACAAGTTTTGATCAGCAAAATAAACAGCATTTCTTGTTTTGGAAACAAAA

204/550

FIGURE 204

MRSVQIFLSQCRILLLLLVPTMLLKS LGEDVIFHPEGEFDSYEVTIPEKLSFRGEVQGVVSPVS
 YLLQLKGKKHVLHLWPKRLLLPRHLRVFSFTEHGELLEDPYIPKDCNYMGSVKESLDSKATI
 STCMGGLRGVFNIDAKHYQIEPLKASPSFEHVVYLLKKEQFGNQVCGLSDDEIEWQMAPYENK
 ARLRDFPGSYKHPKYLELILLFDQSRYRFVNNNLSQVIHDAILLTGIMDTYFQDVRMRIHLKA
 LEVWTFDNKIRVGYPELAEVLGRFVIYKKSVLNARLSSDWAHLYLQRYNDALAWSFGKVCSL
 EYAGSVSTLLDTNILAPATWSAHELGHAVGMSHDEQYCQCRGRLNCIMGSGRTGFSNCSYISF
 FKHISSGATCLNNIPGLGYVLKRCGNKIVEDNEECDGSGTEECQKDRCCQSNCKLQPGANCSI
 GLCCHDCRFRPSGYVCRQEGNECDLAEYCDGNSSSCPNDVYKQDGTFCYEGRCFRKGCRSRY
 MQCQSIFGPDAMEAPSECYDAVNLIQDQFGNCEITGIRNFKKCESANSICGRLQCINVETIPD
 LPEHTTIIISTHLQAENLMCWGTGYHLSMKPMGIPDLGMINDGTSCGEGRVCFKKNVCNSSVLQ
 FDCLPEKCNTRGVCNNRKNCHCMYGWAPPFCEEVGYGGSIDSGFPGLLRGAIPSSIWVVSIIIM
 FRLILLILSVVFVFFRQVIGNHLKPKQEKMPLSKAKTEQEESKTKTVQEESKTKTGQEESEAK
 TGQEESKAKTGQEESKANIESKRPAKSVKKQKK

Signal peptide:

amino acids 1-27

Transmembrane domain:

amino acids 684-705

N-glycosylation sites.

amino acids 222-226, 372-376, 438-442, 473-477, 625-629

N-myristoylation sites.
 amino acids 131-137, 168-174, 235-241, 319-325, 364-370, 436-442,
 472-478, 609-615, 642-648, 668-674, 676-680, 680-686, 749-755,
 758-764, 767-773
Amidation site.

amino acids 69-73

Disintegrins proteins

amino acids 429-479

EGF-like domain proteins

amino acids 650-662

Neutral zinc metallopeptidases, zinc-binding region proteins

amino acids 335-345

205/550

FIGURE 205

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGGGAAGGTTGAATGGGGTAGAAGGCCTG
TTGTGGAGGGAAACCACCCATCCTCCTGCCTCCCACCACCACCATCATCCTGGCTGGACGGAG
AGGGTGACGGGGGCTGGGAAGGGGCAGCTCATGTTTCAGGTTTCCAGGAGGGGCTACCTGTTGA
CTGTCTTTGCAGGAAGAAGAAAAACCTGAGTGACCAGATGTCCCAGCTCCAGGTGCCTTGCC
AGATGGCCAGAACCACACCTCTTGAAGAGTGACAGTGCTGTGGAGCATGGTTTTCTGCACACCT
GGAATGACTGGAACCCCAAGACTCAAGAAGGAGCTAAAGATCTTGAAGTAGACATGAATAAA
ACAGAAGGCTGTGGACCACCTGTGAGATGGAGAAGTCCTTCTGAGGCTATCCAAACACGGAC
CAGGCCATGAGACCCCGATGACCATCCCTGAATTTTTTCGAGAGTCAGTCAACCGATTTGGAA
CTTATCCAGCCCTCCCATCCAAGAATGGCAAAAAGTGGGAAATTCTGAATTTCAACCAGTACT
ATGAGGCTTGTGGAAGGCTGCAAAATCCTTGATCAAGCTGGGTTTGGAGCGTTTCCACGGAG
TTGGTATCCTGGGGTTTAACTCTGCAGAGTGGTTTATCACTGCTGTTGGTGCCATCCTAGCCG
GGGGTCTTTGTGTTGGTATTTATGCCACCAACTCTGCCGAGGCTTGTCAATATGTCATCACTC
ATGCCAAAGTGAACATCTTGCTGGTTGAGAATGATCAACAGTTACAGAAAATCCTTTCGATTC
CACAGAGCAGCCTAGAGCCCCCTAAAAGCGATCATCCAGTACAGACTGCCAATGAAGAAGAACA
ACAACCTTGACTCTTGGGATGATTTTCATGGAACCTTGGCAGAAGTATCCCTGACACCCAACTGG
AGCAGGTCATCGAGAGCCAGAAGGCCGAATCAATGCCGAGTGCTCATCTACACTTCAGGGACCA
CAGGCATACCCAAGGGAGTGATGCTCAGTCATGACAACATCACGTGGATTGCAGGAGCAGTGA
CAAAGGACTTTAACTGACAGACAAGCATGAGACGGTGGTTAGCTACCTCCCACTCAGCCATA
TTGCAGCACAGATGATGGACATCTGGGTACCCATAAAGATTGGGGCGCTCACATACTTTGCTC
AAGCAGATGCTCTCAAGGGCACCTTGGTAAGTACTCTAAAGGAGGTAAAACCTACTGTCTTCA
TTGGAGTGCCTCAAATTTGGGAGAAGATACATGAGATGGTGAAGAAAAATAGTGCCAAGTCCA
TGGGCTTGAAGAAGAAGGCATTCGTGTGGGCAAGAAACATTGGCTTCAAGGTCAACTCAAAAA
AGATGTTGGGGAAATATAATACTCCCGTGAGCTACCGCATGGCTAAGACTCTCGTGTTTCAGCA
AAGTCAAGACATCCCTTGGCTTGGATCACTGTCACTCTTTTATCAGTGGGACTGCGCCCCCTCA
ACCAAGAGACTGCCGAGTTCTTTCTAAGCTTGGACATACCTATAGGCGAGTTGTATGGGTGGA
GTGAGAGCTCGGGACCCACACGATATCCAACCAGAATAACTACAGGCTTCTAAGCTGTGGCA
AGATCTTGACTGGGTGTAAGAATATGCTGTTCCAGCAGAACAAGGATGGCATTGGGGAGATCT
GCCTCTGGGGTAGGCACATCTTCATGGGCTATCTGGAAAGTGAGACTGAAACTACAGAGGCCA
TCGATGATGAAGGCTGGCTACACTCTGGGGATCTGGGCCAGCTGGACGGTCTGGGTTTCTCTCT
ATGTCACCGGCCACATCAAAGAAATCCTTATCACTGCTGGTGGTGAAGTGTGCCCCCATTC
CTGTTGAGACCTTGGTTAAGAAGAAGATCCCCATCATCAGTAACGCCATGTTAGTAGGAGATA
AACTGAAGTTTCTGAGCATGTTGCTGACGCTGAAGTGTGAGATGAATCAGATGAGCGGAGAAC
CTCTGGACAAGCTGAACTTCGAGGCCATCAACTTCTGTGGGGTCTGGGCAGCCAGGCATCCA
CCGTGACTGAGATTGTGAAGCAGCAAGACCCCTGGTCTACAAGGCCATCCAGCAAGGCATCA
ATGCTGTGAACCAGGAAGCCATGAACAATGCACAGAGGATTGAAAAGTGGGTCATCTTGGAGA
AGGACTTTTCCATCTATGGTGGAGAGCTAGGTCCAATGATGAAACTTAAGAGACATTTTGTAG
CCCAGAAATACAAAAACAAATTGATCACATGTACCACTGACTGCTTTGATGGAGCTGCTCTC
AGCTGTTCTGATGCCTTCAGCAGGAAGACCTCATTGCAATAAGTGAAATGCTGCTCTAGGTAG
AAGCTCTCCCTGCTGTTTTTAAGAAGCCACATTCCTCATTGGTCAGTTTCTTGATTGTTCTGTC
TGTTGGAGAGGTGCTCCCTAGAAGAACCTGCCATACGTTTCAAAGCAATAAAATCACTGTATA
TCTTTCTAAGGACCTTCAAGTCATGACTCCAGGGAAGCCTATTGGGAAGTCTACTAAAACTG
CCTGATTTACAAGAAAGACCTGAACTTGTGGGCTCCCATTTGATTTTTTCTCCTCAGGGGAC
TCAGACATTAGAAAGAAAAAGCCTCACAGATTTGAAGAAGTGGACCCCCAAATCAACTCACCT
GCCTGGAAGCAACTGGGAAACCCCTTCCAATAAGTCCTGATAATAAAGCACTTCAGGGTCCCAA
AAAAA

206/550

FIGURE 206

MTIPEFFRESVNRFGTYPALPSKNGKKWEILNFNQYYEACRKAAKSLIKLGLERFHGVGILGF
NSAEWFITAVGAILAGGLCVGIYATNSAEACQYVITHAKVNILLVENDQQQLQKILSIPQSSLE
PLKAI IQYRLPMKKNNNLYSWDDFMELGRSIPDTQLEQVIESQKANQCAVLIYTS GTTGIPKG
VMLSHDNITWIAGAVTKDFKLTDKHETVVSYLPLSHIAAQMMDIWVPIKIGALTYFAQADALK
GTLVSTLKEVKPTVFIGVPQIWEKIHVMVKNSAKSMGLKKKAFVWARNIGFKVNSKKMLGKY
NTPVSYRMAKTLVFSKVKTS LGLDHCHSFISGTAPLNQETAEFFLSLDIPIGELYGLSESSGP
HTISNQNNYRLSCGKILTGCKNMLFQQNKDGIGEICLWGRHIFMGYLESETETTEAIDDEGW
LHSGDLGQLDGLGFLYVTGHIKEILITAGGENVPPIPVETLVKKKIPIISNAMLVGDKLKFLS
MLLTLKCEMNQMSGEPLDKLNFEAINFCRGLGSQASTVTEIVKQQDPLVYKAIQQGINAVNQE
AMNNAQRIEKWVILEKDFSIYGGELGPMMLKKRHFVAQKYKKQIDHMYH

Signal peptide:

amino acids 1-22

Transmembrane domain:

amino acids 65-86

N-glycosylation site.

amino acids 196-200

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 282-286

Tyrosine kinase phosphorylation sites.

amino acids 547-555, 608-616

N-myristoylation sites.amino acids 15-21, 74-80, 80-86, 84-90, 185-191, 189-195,
253-259, 337-343, 371-377, 448-454, 536-542**Amidation site.**

amino acids 24-28

Putative AMP-binding domain signature.

amino acids 177-189

Putative AMP-binding domain proteins.

amino acids 173-190

207/550

FIGURE 207

CCCACGCGTCCGCCCACGCGTCCGCGGACGCGTGGGGCCAGATCGCGGCCGGCGCCAGCGCCA
CCGTCCGGTCCACCCGCCAGCCCGCACAGCCGCGCCGCCGAGCGTTTCGTGAGCGGCGCT
CCGAGGATCAGGAATGGGGCTTCGGGCGCTGGGCGCGCTCCGAACCCGGCGCACGTAAGAGCC
TGGGAGCGCCCGAGCCGCGCCGGCTGCCCGGAGCCCCATCGCCTAGGACCGGGAGATGCTGGAA
ATGCAACCGCCTGTTCCCCGAGGAGCCGCTGCCCCCGGACCCCCCTGGCACTGTGCGCACCTT
GGTCAGCAGCCCCCGGAGAAGACGGCGCCCCCAACGCCCGACCCGCGTGGCCGTGGCAGCGCC
ACGCGAGCCCTCTAGGCGACCCGAGGGCCACAGCAGCTCAGCCGCCGGTGGCCCCCTCGGAAAC
CATGACCCCCGGCGCGGGCCCATGGAGCCATGGCCTATAGGGTCCCTGGGCGCGCGGGGCCAC
CTCAGCCGCGGAGGGCGCGCAGGCTGCTCTTCGCCTTCACGCTCTCGCTCTCCTGCACTTACC
TGTGTTACAGCTTCCTGTGCTGCTGCGACGACCTGGGTGCGAGCCGCTCCTCGGCGCGCCTC
GCTGCCTCCGCGGCCCCAGCGCGGGCGGCCAGAACTTCTCCAGAAGTCCCGCCCCCTGTGATC
CCTCCGGGCCGACGCCCAGCGAGCCCAGCGCTCCAGCGCGCCCGCCGCGCCGTGCCCGCCC
CTCGCCTCTCCGGTTCCAACCACTCCGGCTCACCCAAGCTGGGTACCAAGCGGTTGCCCAAG
CCCTCATTTGTGGGCGTGAAGAAGGGGGGACCCGGGCCGTGCTGGAGTTTATCCGAGTACACC
CGGACGTGCGGGCCTTGGGCACGGAACCCCACTTCTTTGACAGGAACTACGGCCGCGGGCTGG
ATTGGTACAGGAGCCTGATGCCCAGGACCCCTCGAGAGCCAGATCACGCTGGAGAAGACGCCCA
GCTACTTTGTCACTCAAGAGGCTCCTCGACGCATCTTCAACATGTCCCGAGACACCAAGCTGA
TCGTGGTTGTGCGGAACCCCTGTGACCCGTGCCATCTCTGATTACACGCAGACACTCTCCAAGA
AGCCCGACATCCCGACCTTTGAGGGCCTCTCCTTCCGCAACCCGACCCCTGGGCCTGGTGGACG
TGTCATGGAACGCCATCCGCATCGGCATGTACGTGCTGCACCTGGAGAGCTGGCTGCAGTACT
TCCCGCTAGCTCAGATTCACTTCGTCACTGGCGAGCGACTCATCACTGACCCGGCCGGCGAGA
TGGGGCGAGTCCAGGACTTCCTGGGCATTAAGAGATTCATCACGGACAAGCACTTCTATTTCA
ACAAGACCAAAGGATTCCCTTGCTTGAAAAAACAGAATCGAGCCTCCTGCCTCGATGCTTGG
GCAAATCAAAGGGGAGAACTCATGTACAGATTGATCCTGAAGTGATAGACCAGCTCCGAGAAT
TTTATAGACCGTATAATATCAAATTTTATGAAACCGTTGGGCAGGACTTCAGGTGGGAATAAG
CCCACGAAAGGAAAGGGCTCTCAAGGGCTCTTCTGCTCATCTCTTCCGTGAGATTTGCTCCCA
GACCCTCTGATCTCCCTCCAACAAACCTGGCTCCAGCCCCCTTTCCCAACTTGAGTTGCATC
ATCTTGGAACCAGGAAGCCCAGCTAAAGCCAAGAGACCAGAGAGTCCCAGCACTAGTTTTCA
TCAGTCTGTTCAAGCAAAGTTGATCTGCTCCTGGCACGTCCAGTAAATTCAGAATCATTCTC
CTTTCTGCCATAAAGGGCCTTGGAGAATTGCTTTAAGAAGAGTGAATGTTCCAATGATGATA
GATATTATAAGCGATGATGGTTCTGTTGCTATGAACACAGCAGTCGGTCCCTGTCAATTGTCCA
CCCAGGAGTGGCCTTGTTAATTCCAAGTGGCATGTATCTTCCCTCTGAGCTTCATTTCTTCAA
GATGCTCTGGGTGGTGGGATGGGAGACCATCCTCAGCCCTCCTCAGACCTTATCAATTCATTG
AGAGATTGCAAAGCTGAAAGCACCTCCGGCCACTCCTGGGAGACAGACCCTTTGGTGATGAAA
TAAACCAGTGACTTCAGAGCCTATGGTCTCAACTGTGCTTGAAAACACTGTCTCTGAAAAA
ACTTTGTGATTCTCCCTGCTCCCTGTGGACAAAAGCACATAATTCTGCTGTTACGGGTACTTT
GCTCATACGAGCTTTCATGTTACGATGCAATGGAATCATGCTTGTCATGTGAAATAAATAT
GGCTCTCTCGTGTCTTAATGCTGGGCTTTTCTCTGTAAGCTGGTTCTGCAGCACAATTCATT
AATTAACTTCTCCAGTGCAAGAAGGCAGCTGGTGCTGGGGGTGGTCTGGGGGGTCAGGGAG
GAGGGCAAGGACTACATGGGGCAGAGGCAAGGCGGTGGTGGAGATGAGGAAAGAAGTTCTTCT
TGGCAGAAGCTGGGGCAGAAAGATCACATGAGATCTGTGGGGACACCCTCTATCTGAAACATA
AGTCTGTGTTCACTCTCTGCTTAGAAATTTTAGATCTGAAGTGCTACACTGAAGGTCCGAAGG
TTGATGGGGCATCAGATATCTTTTTGGTTGGCCAGCATGATATTTTGAAATAACTGTCAACAG
TTAGAACTGGGAGCATTCATATGTAAAAAATATGGATTTTCAGCTTCTTCTTAAAAA
AAAAA
AAAAA

208/550

FIGURE 208

MAYRVLGRAGPPQPRRARLLFAFTLSLSCTYLCYSFLCCDDLGRSRLLGAPRCLRGPSAGG
QKLLQKSRPCDPSGPTPSEPSAPSAPAAVPAERLSGSNHSGSPKLGTKRLPQALIVGVKKGG
TRAVLEFIRVHPDVRLGTEPHFFDRNYGRGLDWYRSLMPRTLESQITLEKTPSYFVTQEAPR
RIFNMSRDTKLIVVVRNPVTRAISDYTQTLSSKKPDIPTFEGLSFRNRTLGLVDVSWNAIRIGM
YVLHLESWLQYFPLAQIHVFSGERLITDPAGEMGRVQDFLGIKRFITDKHFYFNKTKGFPCLK
KTESSLLPRCLGKSKGRTHVQIDPEVIDQLREFYRPYNIKFYETVGQDFRWE

Signal peptide:

amino acids 1-33

N-glycosylation sites.

amino acids 102-106, 193-197, 235-239, 306-310

Tyrosine kinase phosphorylation site.

amino acids 296-305

N-myristoylation sites.

amino acids 51-57, 100-106, 121-127, 125-131

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 20-31

209/550

FIGURE 209

CTTTCCTTATCTGTGTGTACTCTTATCTCACTGTTCTATTTTTTCTCCTCATTTATATTA
CTTTCCTTACCTTTTTTTCTGAACCTTCTAGGCCTTCTCTTTCCAGAACTGGTGAAGACAAATG
AAACGGCCAAGATGGTAAGAAACAAGCCGCATTTCTCCTTGGGGAGACTGATAATTTAAAAGG
TTTGTGTGTGTCAGAAACATTTCCAGCTTCATCACCAACCCTTTCCTTCCACCTCTGCCCCACTG
GAGACCACTTACATCCCGAAGCGGACGCGGCAGCTGAAGTCAGGAAACCATGCATCACATTAG
CAGGAGCCAACTGCAGACTTTAAACTCCGTTCAACATGTGGATGCGGCAGAGAAATGACCTGT
CCAGACAAGCCGGGGCAGCTCATAAACTGGTTCATCTGCTCCCTGTGCGTCCCGCGGGTGCCT
AAGCTCTGGAGCAGCCGGCGTCCAAGGACCCGGAGAAACCTTCTGCTGGGCACTGCGTGTGCC
ATCTACTTGGGCTTCCCTGGTGAGCCAGGTGGGGAGGGCCTCTCTCCAGCATGGACAGGCGGCT
GAGAAGGGGCCACATCGCAGCCGCGACACCGCCGAGCCATCCTTCCCTGAGATACCCCTGGAT
GGTACCCTGGCCCCCTCCAGAGTCCCAGGGCAATGGGTCCACTCTGCAGCCCAATGTGGTGTAC
ATTACCCTACGCTCCAAGCGCAGCAAGCCGGCCAATATCCGTGGCACCGTGAAGCCCAAGCGC
AGGAAAAAGCATGCAGTGGCATCGGCTGCCCCAGGGCAGGAGGCTTTGGTTCGGACCATCCCTT
CAGCCGCAGGAAGCGGCAAGGGGAAGCTGATGCTGTAGCACCTGGGTACGCTCAGGGAGCAAAC
CTGGTTAAGATTGGAGAGCGACCCTGGAGGTTGGTGCGGGGTCCGGGAGTGCGAGCCGGGGGC
CCAGACTTCCTGCAGCCCAGCTCCAGGGAGAGCAACATTAGGATCTACAGCGAGAGCGCCCCC
TCCTGGCTGAGCAAAGATGACATCCGAAGAATGCGACTCTTGCGGACAGCGCAGTGGCAGGG
CTCCGGCCTGTGTCTCTAGGAGCGGAGCCCGTTTGTCTGGTGTGGAGGGGGGCGCACCTGGC
GCTGTGCTCCGCTGTGGCCCTAGCCCTGTGGGCTTCTCAAGCAGCCCTTGGACATGAGTGAG
GTGTTTGCCTTCCACCTAGACAGGATCCTGGGGCTCAACAGGACCCTGCCGTCTGTGAGCAGG
AAAGCAGAGTTTCATCCAAGATGGCCGCCCATGCCCATCATTCTTTGGGATGCATCTTTATCT
TCAGCAAGTAATGACACCCATTCCTTCTGTTAAGCTCACCTGGGGAACCTTATCAGCAGTTGCTG
AAACAGAAATGCTGGCAGAATGGCCGAGTACCCAAGCCTGAATCAGGTTGTACTGAAATACAT
CATCATGAGTGGTCCAAGATGGCACTCTTTGATTTTTTGTACAGATTTATAATCGCTTAGAT
ACAAATTGCTGTGGATTTCAGACCTCGCAAGGAAGATGCCTGTGTACAGAATGGATTGAGGCCA
AAATGTGATGACCAAGGTTCTGCGGCTCTAGCACACATTATCCAGCGAAAGCATGACCCAAGG
CATTTGGTTTTTTATAGACAACAAGGGTTTCTTTGACAGGAGTGAAGATAACTTAACTTCAAA
TTGTTAGAAGGCATCAAAGAGTTTCCAGCTTCTGCAGTTTCTGTTTTGAAGAGCCAGCACTTA
CGGCAGAAACTTCTTCAGTCTCTGTTTCTTGATAAAGTGTATTGGGAAAGTCAAGGAGGTAGA
CAAGGAATTGAAAAGCTTATCGATGTAATAGAACACAGAGCCAAAATTTCTTATCACCTATATC
AATGCACACGGGGTCAAAGTATTACCTATGAATGAATGACAAAAGAATCTTCTGGCTAGGGTG
TTAGATATATTTATGCATTTTTGGTTTTGTTTTTAAATCAAGCACATCAACCTCAAGCCCGTT
TAGCAATGAGGCAGTGTAGATGAATACGTAAAATAAATGACTTTAACCAAGTAGCTATAAAGG
GACTTAGCACTGTATGCATACTTAAAAGGTTTTGAAAAACAACTACTTGAGAAATATTTGT
TTATATTTTTCTCTAACATCATGCTATGTGTGAGTCTGAACATCTGACAACAGAAATTTTCACT
TATTATTCTAGCTAAGTTTTGAAAACATTTGTGATGCTGTTTAAATAGAAAACCTGCAAACCAGA
GATACTGACTCCATTAATAAACCATATTTTTGTGCGGTTTTGACTGTTCTGACCAAATACTAAT
GGGAACAATTCTTGACGTTTTTCTGTTGCTGATTGTTAACATAGAGCAGTCTCTACACTACCC
TGAGGCAACTCTACATTGGAACACTGAGGCTTACAGCCTGCAAGAGCATCAGAGCTGACCATA
CATTTAAACAGAAATGCTGGTTTTATTTGCAAAATCACCAGTATATTTTCTATTGTGTCTATAA
AAAATCAGTCATTTAAGTACAAGAATCATATTTTCCATTCCTTTTTAGAAATTTATTTTGTG
TCCCTATGGAAATCATTACATCTGACAATTTATATGTTAAAGAGTTTTACTCTCTCTATTTT
GGTCCAATTTGTATCTAGTGGCTGAGAAATTAAATAATTCTAAAGTATGAAGTTACCTATCTG
AAAATGTACTTACAGAGTATCATTTTAAATGGATGTCTCTTTAAAAATTTTGTACTTTTAC
CAACAATGTAATATAATTTATGTATATTTTATTAATAATAGTGAATTCCTTAAATTTGTTCT
ATGTACTTATATTTAATTTGATTTAATGGTTACTGCCAGATATTGAGAAATGGTTCAATAT
TGAGTGTGTTTCAATAA

210/550

FIGURE 210

MTCPDKPGQLINWFICSLCVPRVRKWLWSSRRPRTRRNLLLGTACAIYLGFLVSQVGRASLQHG
QAAEKGPHRSDTAEPSFPEIPLDGTLAPPESQGNGSTLQPNVVYITLRSKRSPANIRGTVK
PKRRKKHAVASAAPGQEAALVGPSLQPQEAAREADAVAPGYAQGANLVKIGERPWRLVRGPGVR
AGGPDFLQPSSRESNIRIYSESAPSWLSKDDIRRMRLADS AVAGLRPVSSRSGARLLVLEGG
APGAVLRCGPSPCGLLKQPLDMSEVFAFHLDRI LGLNRTLPSVSRKAEFIQDGRPCPIILWDA
SLSSASNDTHSSVKLTWGTYYQQLLKQKCWQNGRVKPKPESGCTEIHHEWSKMALEDFLLQIYN
RLDTNCCGFRPRKEDACVQNGLRPKCDDQGSAA LAHIIQRKHDPRHLVFIDNKGFFDRSEDNL
NFKLLEGIKEFPASAVSVLKSQHRLRQKLLQSLFLDKVYWESQGGROGIEKLIDVIEHRAKILI
TYINAHGVKVLPMNE

Transmembrane domain:

amino acids 40-56

N-glycosylation sites.

amino acids 98-102, 289-293, 322-326

N-myristoylation sites.amino acids 8-14, 41-47, 97-103, 187-193, 251-257, 252-258,
287-293, 484-490

211/550

FIGURE 211

GTGGGGTGGTGAGCGCAGCGCCGAGGATGAGGAGGTGCAACAGCGGCTCCGGGCCGCCCGCTCGCTGCTGCTGC
TGCTGCTGTGGCTGCTCGCGGTTCCCGGCGTAACCGCGGCCCGGGTCCGGCGCTCTATTGCGCTTCCGACCCGC
TGACGCTGCTGCAGGCGGACACGGTGCGCGGCGCGGTGCTGGGCTCCCGCAGCGCTGGGCCGTGGAGTTCTTCG
CCTCCTGGTGCGGCCACTGCATCGCCTTCGCCCCGACGTGGAAGGCGCTGGCCGAAGACGTCAAAGCCTGGAGGC
CGGCCCTGTATCTCGCGCCCTGGACTGTGCTGAGGAGACCAACAGTGCAGTCTGCAGAGACTTCAACATCCCTG
GCTTCCCGACTGTGAGGTTCTTCAAGGCCTTTACCAAGAACGGCTCGGGAGCAGTATTTCCAGTGGCTGGTGCTG
ACGTGCAGACGCTGCGGGAGAGGCTCATTGACGCCCTGGAGTCCCATCATGACACGTGGCCCCCAGCCTGTCCCC
CACTGGAGCCTGCCAAGCTGGAGGAGATTGATGGATTCTTTGCGAGAAATAACGAAGAGTACCTGGCTCTGATCT
TTGAAAAGGGAGGCTCCTACCTGGGTAGAGAGGTGGCTCTGGACCTGTCCAGCACAAAGGCGTGGCGGTGCGCA
GGGTGCTGAACACAGAGGCCAATGTGGTGAGAAAGTTTGGTGTACCGACTTCCCTCTTGCTACCTGCTGTTCC
GGAATGGCTCTGTCTCCGAGTCCCGTGTCTATGGAATCCAGGTCTTCTATACCGCTTACCTGCAGAGACTCT
CTGGGCTCACCAGGGAGGCTGCCCAGACCACAGTTGCACCAACCACTGCTAACAAGATAGCTCCCACTGTTTGA
AATTGGCAGATCGCTCCAAGATCTACATGGCTGACCTGGAATCTGCACTGCCTACATCCTGCGGATAGAAGTGG
GCAGGTTCCCGGCTCCTGGAAGGCGAGCGCCTGGTGGCTTGAAAAAGTTTGTGGCAGTGTGGCCAAGTATTTCC
CTGGCCGGCCCTTAGTCCAGAACTTCTGCACTCCGTGAATGAATGGCTCAAGAGGCAGAAGAGAAATAAAATTC
CCTACAGTTTCTTTAAACTGCCCTGGACGACAGGAAAGAGGGTGCCGTTCTTGCCAAGAAGGTGAAGTGGATTG
GCTGCCAGSGGAGTGAGCCGCATTTCCGGGGCTTCCCTGCTCCCTGTGGGTCTCTTCCACTTCTTGAAGTGTG
AGGCAGCTCGGCAAAATGTAGACCACTACAGGAAGCAGCCAAAGGCCAAGGAGGTCTCCAGCCATCCGAGGCT
ACGTGCCTACTTCTTCCGCTGCCGAGACTGCGCTAGCCACTTCGAGCAGATGGCTGCTGCCCTCCATGCACCGGG
TGGGGAGTCCCAACGCCGCTGTCTCTGGCTCTGGTCTAGCCACAAACAGGGTCAATGCTCGCCTGCAGGTGCC
CCAGCGAGGACCCCCAGTTCCCCAAGGTGCAGTGGCCACCCCTGAAGTTTGTCTGCTGCCACAATGAACGCC
TGGATGTGCCCTGTGGGACGTGGAAGCCACCTCAACTTCTCAAGGCCACTTCTCCCCAAGCAACATCATCC
TGGACTTCCCTGCAGCTGGGTGAGTGTGCCCGAGGGATGTGCAGAAATGTGGCAGCCGCCCCAGAGCTGGCGATGG
GAGCCCTGGAGCTGGAAGCCCGGAATTCAACTCTGGACCTTGGGAAGCCTGAGATGATGAAGTCCCCCACAACA
CCACCCACATGTGCCGGCTGAGGGACCTGAGGCAAGTGCACCCCCGAGCTGCACCTTGGCCTCAGAGCTGCAC
CAGGCCAGGAGCCTCCTGAGCACATGGCAGAGCTTCAGAGGAATGAGCAGGAGCAGCCGCTTGGGCAGTGGCACT
TGAGCAAGCGAGACACAGGGCTGCATTGCTGGCTGAGTCCAGGGCTGAGAAGAACCCTCTGGGGCCCTTTGG
AGGTGAGGCGCGTGGGCCGAGCTCCAAGCAGCTGGTGCACATCCCTGAGGGCCAGCTGGAGGCCCCGAGCTGGAC
GGGGCCGAGGCCAGTGGCTGCAGGTGCTGGGAGGGGGCTTCTCTTACCTGGACATCAGCCTCTGTGTGGGGCTCT
ATTCCCTGTCTTTCATGGGCTGCTGGCCATGTACACCTACTTCCAGGCCAAGATAAGGGCCCTGAAGGGCCATG
CTGGCCACCCCTGCAGCTTGAACACCTGGGGAGGAGCGGGAGAGGGAGCTGCCATCTCTAGGCACCTCAAGCCC
CCTGACCCCATTCCTCCCTCCCAACCCCTTGTCTTGTCTGGCCTAGAAAGTGTGGGAAATTGAGGAAAACGAG
TTGCTCCAGTGAAGCTTCTTGGGGTTGCTAGGACAGAGAGCTCCTTTGACACAAAAGACAGGAGCAGGGTCCAGG
TTCCCTGCTGTGCAGGGAGGGCAGCCCCGGGCAGTGGGCATAGGGCAGCTCAGTCCCTGGCCTCTTAGCACAC
ATTCTGTTTTTTCAGCTTATTTGAAGTCTGCTCATTCTCACTGGAGCCTCAGTCTCTCTGCTTGGTCTTGGC
CCTCAACTGGGGCAAGTGAAGCCAGAGGAGGTCCCCAGCTGGGTGGGCTGGAATGGAAGTCTCACTAGCTGC
TGGGGCTCCGCCACCCCTGCTCCCTTCCGGACAATGAAGAAGCCTTTGCACCCCTGGGAGGAAGGACCACCCCGG
CCCTCTATGCTTGGCCAGCCTCCAGCTCCTCAGACCTCCTGGGTGGGGTTTGGCTTCAGGGTGGGGTTTGAAGC
TTCTGGAAGTCTGCTGGTCTCCAGGTGAGGCAAGCCATGGTTGCTGGGCTGTAGGGTGAAGTGGCTTGGTGGT
GGGACCTGACGAGTTGGTGGCATGGGAAGGATGTGGGTCTCTAGTGCCTTGGCCTGGCTTAGCTGCAGGAGAAGA
TGGCTGCTTTCACTTCCCCCATTTAGCTCTGCTCCCTCTGAGCCTGGTCTTTTGTCTTTTTTATTTTGGTCTC
CAAGATGAATGCTCATCTTTGGAGGGTGCCAGGTAGAAGCTAGGGAGGGGAGTGTCTTCTCTCTCCAGGTTTCAC
CTTCCAGTGTGCAGAAAGTTAGAAGGGTCTGGCGGGGCGAGTGCCTTACACATGCTTGATTCCACGCTACCCCT
GCCTTGGGAGGTGTGTGAATAAATTATTTTCTTAAGCA

212/550

FIGURE 212

MRRCN SGSGPPPSLLLLLLWLLAVPGANAAPRSALYSPSDPLTLLQADTVRGAVLGSRSAWAV
EFFASWCGHCIAFAPTWKALAEDVKAWRPALYLAALDCAEETNSAVCRDENIPGFPTVREFKA
FTKNGSGAVFPVAGADVQTLRERLIDALESHHDTWPPACPPLEPAKLEEIDGFFARNNEEYLA
LIFEKGGSYLGREVALDLSQHKGVAVRRVLNTEANVVRKFGVTDFFPCYLLFRNGSVSRVPVL
MESRSFYTAYLQRLSGLTREAAQTTVAPTANKIAPT VWKLADRSKIYMADLESALHYILRIE
VGRFPVLEGQRLVALKKFVAVLAKYFPGRPLVQNFLHSVNEWLKRQKRNKIPYSFFKTALDDR
KEGAVLAKKVNWIGCQGSEPHFRGFPCSLWVLFHFLT VQAARQNVDSQEAAKAKEVLPAIRG
YVHYFFGCRDCASHFEQMAAASMRVGS PNAAVLWLWSSHNRVNARLAGAPSEDPQFPKVQWP
PRELCSACHNERLDVPVWDVEATLNFLKAHFS PNIILDFPAAGSAARRDVQNVAAPELAMG
ALELESRNSTLDPGKPEMMKSPTNTT PHVPAEGPEASRPFKLHPGLRAAPGQEPPEHMAELQR
NEQEQLGQWHLSKRDTGAALLAESRAEKNRLWGPLEVRRVGRSSKQLVDIPEGQLEARAGRG
RGQWLQVLGGGFSYLDISLCVGLYSLSF MGLLAMTYTFQAKIRALKGHAGHPAA

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 705-728

N-glycosylation sites.

amino acids 130-134, 243-247, 575-579

Glycosaminoglycan attachment site.

amino acids 6-10

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 644-648

N-myristoylation sites.amino acids 52-58, 56-62, 196-202, 381-387, 392-398, 448-454,
468-474, 684-690, 702-708**Cytochrome c family heme-binding site signature.**

amino acids 509-515

Thioredoxin family proteins

amino acids 62-78

213/550

FIGURE 213

GCACGAGGCCGACTTCCAGACCATCTACAACCTGCACGGCCTGGAACAGCTTCGGCTCCGACAC
TGAGATCATCCGGCTCAAGGAGCAAGGTTTCGGAAATGAAGTCGGGAGCCGGGCTGGAAGCAGA
GTCTGTGCCG**ATG**GCCGTCATCATTGGGGTGGCCGTAGGAGCTGGTGTGGCCTTCCTCGTCCT
TATGGCAACCATCGTGGCGTTCTGCTGTGCCCGTTCCAGAGAAATCTCAAAGGTGTTGTGTC
AGCCAAAATGATATCCGAGTGGAATTTGTCCACAAGGAACAGCCTCTGGTCGGGAGGGTGA
GGAGCACTCCACCATCAAGCAGCTGATGATGGACCGGGGTGAATTCAGCAAGACTCAGTCCT
GAAACAGCTGGAGGTCCTCAAAGAAGAGGAGAAAGAGTTTCAGAACCTGAAGGACCCACCAA
TGGCTACTACAGCGTCAACACCTTCAAAGAGCACCCTCAACCCCGACCATCTCCCTCTCCAG
CTGCCAGCCCGACCTGCGTCCTGCGGGTAAGCAGCGTGTGCCACAGGCATGTCTTCACCAA
CATCTACAGCACCTGAGCGGCCAGGGCCGCCTCTACGACTACGGGCAGCGGTTTGTGCTGGG
CATGGGCAGCTCGTCCATCGAGCTTTGTGAGCGGGAGTTCCAGAGAGGCTCCCTCAGCGACAG
CAGCTCCTTCCTGGACACGCAGTGTGACAGCAGCGTCAGCAGCAGCGGCAAGCAGGATGGCTA
TGTGCAGTTCGACAAGGCCAGCAAGGCTTCTGCTTCCTCCTCCCACCACTCCCAGTCCTCGTC
CCAGAACTCTGACCCCGAGTCGACCCCTGCAGCGGCGGATGCAGACTCACGTC**TAAG**GATCACA
CACCGCGGGTGGGGACGGGCCAGGGAAGAGGTCAGGGCACGTTCTGGTTGTCCAGGGACGAGG
GGTACTTTGCAGAGGACACCAGAATTGGCCACTTCCAGGACAGCCTCCCAGCGCCTCTGCCAC
TGCCTTCCTTCGAAGCTCTGATCAAGCACAAATCTGGGTCCCAGGTGCTGTGTGCCAGAGGT
GGGCGGGTGGGGAGACAGACAGAGGCTGCGGCTGAGTGCGCTGTGCTTAGTGCTGGACACCCG
TGTCCCCGGCCCTTTCTGGAGGCCCTCTACCACCTGCTCTGCCACAGGCACAAGTGGCAG
CTATAACTCTGCTTTCATGAAACTGCGGTCCACTCTCTGGTCTCTCTGTGGGCTCTACCCCTC
ACTGACCACAAGCTCTACCTACCCCTGTGCCTGTGCTCCCATACAGCCCTGGGGAGAAGGGGA
TGACGTCTTCCAGCACTGAGCTGCCCCAGAAACCCCGGCTCCCCACTGCTGCTCATAGCCCA
TACCCTGGAGGCTGACAAGCCAGAAATGGCCTTGGCTAAAGGAGCCTCTCTCTCACCAGGCTG
GCCGGGAGCCCACCCCAATTTGTTTGGTGTTTTGTGTCCATACTCTTGCAAGTTCTGTCTTG
GACTTGATGCCGCTGAACTCTGCGGTGGGACCGGTCCCGTCAGAGCCTGGTGTACTGGGGGGA
GGGAGGGAGGAGGGAGCCTGTGCTGACGGAGCACCTCGCCGGGTGTGCCCCCTCTGGGCTGTG
TGACCCAGCCTCCCCACCCACCTCCTGCTTTGTGTACTCCTCCCCCTCCCCCTCAGCACAAATC
GGAGTTCATATAAGAAGTGCGGGAGCTTCTCTGGTCAGGGTTCTCTGAACACTTATGGAGAGA
GTGCTTCCTGGGAAGTGTGGCGTTTGAAGGGGCTGGAGGGCAGGTCTTTAAGATGGCGAGACT
GCCCTTCTCAGCTGATAAACACAAGAACGGCGATCCTGTCTCAGTAAGGCTCCACGAGAAGA
GAGGAAGTATATCTACACCTCAACCCTCCTAGTCACCACCTGAAATAAATGTTAGGGAAAAAAA

214/550

FIGURE 214

MAVIIGVAVGAGVAFVLVLMATIVAFCCARSQRNLKGVVSAKNDIRVEIVHKEPASGREGEEHS
TIKQLMMDRGEFQQDSVLKQLEVLKEEEKEFQNLKDPTNGYYSVNTFKEHHSTPTISLSSCQP
DLRPAGKQRVPTGMSFTNIYSTLSGQGRLYDYGQRFVLGMGSSSIELCEREFQRGSLSDSSSF
LDTQCDSSVSSSGKQDGYVQFDKASKASASSSSHHSQSSSQNSDPSRPLQRRMQTHV

Signal peptide:

amino acids 1-28

Glycosaminoglycan attachment site.

amino acids 150-154

N-myristoylation sites.

amino acids 6-12, 10-16, 36-42, 139-145, 165-171

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 114-125

215/550

FIGURE 215

CAGCCTTCCTCCCCAGCCTGAGTGACTACTCTATTCCTTGGTCCCTGCTATTGTCGGGGACG
ATTGC**ATG**GGCTACGCCAGGAAAGTAGGCTGGGTGACCGCAGGCCTGGTGATTGGGGCTGGCG
CCTGCTATTGCATTTATAGACTGACTAGGGGAAGAAAACAGAACAAGGAAAAAATGGCTGAGG
GTGGATCTGGGGATGTGGATGATGCTGGGGACTGTTCTGGGGCCAGGTATAATGACTGGTCTG
ATGATGATGATGACAGCAATGAGAGCAAGAGTATAGTATGGTACCCACCTTGGGGCTCGGATTG
GGACTGAAGCTGGAACCAGAGCTAGGGCCAGGGCAAGGGCCAGGGCTACCCGGGCACGTCCGG
CTGTCCAGAAACGGGGCTTCCCCCAATTCAGATGATACCGTTTTGTCCCCTCAAGAGCTACAAA
AGGTTCTTTGCTTGGTTGAGATGTCTGAAAAGCCTTATATTCTTGAAGCAGCTTTAATTGCTC
TGGGTAACAATGCTGCTTATGCATTTAACAGAGATATTATTCGTGATCTGGGTGGTCTCCCAA
TTGTGCGCAAAGATTCTCAATACTCGGGATCCCATAGTTAAGGAAAAGGCTTTAATTGTCCTGA
ATAACTTGAGTGTGAATGCTGAAAATCAGCGCAGGCTTAAAGTATACATGAATCAAGTGTGTG
ATGACACAATCACTTCTCGCTTGAAGTCACTGTGTCAGCTTGCTGGACTGAGATTGCTTACAA
ATATGACTGTTACTAATGAGTATCAGCACATGCTTGCTAATTCCATTTCTGACTTTTTTCGTT
TATTTTCAGCGGGAAATGAAGAAACCAAACCTTCAGGTTCTGAAACTCCTTTTGAATTTGGCTG
AAAATCCAGCCATGACTAGGGAACTGCTCAGGGCCCCAAGTACCATCTTCACTGGGCTCCCTCT
TTAATAAGAAGGAGAACAAGAAGTTATTCTTAACTTCTGGTCATATTTGAGAACATAAATG
ATAATTTCAAATGGGAAGAAAATGAACCTACTCAGAATCAATTCGGTGAAGGTTCACTTTTTT
TCTTTTTTAAAGAATTTCAAGTGTGTGCTGATAAGGTCTGGGAATAGAAAGTCACCATGATT
TTTTGGTGAAAGTAAAAGTTGGAATAATTCATGGCCAACTTGCTGAACATATGTTCCCAAAGA
GCCAGGAAT**TAA**CACCTTGATTTTGTAATTTAGAAGCAACACACATTGTAAACTATTCATTTTC
TCCACCTTGTTTATATGGTAAAGGAATCCTTTCAGCTGCCAGTTTTGAATAATGAATATCATA
TTGTATCATCAATGCTGATATTTAACTGAGTTGGTCTTTAGGTTAAGATGGATAAATGAATA
TCACTACTTGTTCTGAAAACATGTTTGTTGCTTTTTATCTCGCTGCCTAGATTGAAATATTTT
GCTATTTCTTCTGCATAAGTGACAGTGAACCAATTCATCATGAGTAAGCTCCCTTCTGTCATT
TTCATTGATTTAATTTGTGTATCATCAATAAAATTGTATGTTAATGCTGGAAAGA

216/550

FIGURE 216

MGYARKVGVWVTAGLVIGAGACYCIYRLTRGRKQNKKEKMAEGSGDVDDAGDCSGARYNDWSDD
DDDSNESKSIVWYPPWARIGTEAGTRARARARARARATRRRAVQKRASPNSDDTVLSPQELQKV
LCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRDLGGLPIVAKILNTRDPIVEKALIVLNN
LSVNAENQRRLKVYMNQVCDDTITSRLNSSVQLAGLRLLTNMTVTNEYQHMLANSISDEFFRLF
SAGNEETKLQVLKLLLNLAE NPAMTRELLRAQVPSSLGSLFNKKENKEVILKLLVIFENINDN
FKWEENEPTQNQFGEGLFFFLKEFQVCADKVLGIESHHDFLVKVKVGKFMAKLAEHMFPSQE

Signal peptide:

amino acids 1-20

N-glycosylation sites.

amino acids 68-72, 189-193, 217-221, 230-234

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-111

N-myristoylation sites.amino acids 13-19, 17-23, 19-25, 54-60, 83-89, 147-153, 255-261,
290-296**Amidation site.**

amino acids 29-33

FIGURE 217

[illegible]